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OM nucleic - nucleic search, using SW model.

Run on: June 1, 2005, 23:14:35 ; Search time 126.025 Seconds
 (without alignments)

6151.841 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayaatcstrctrgcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : GenEmbl:
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 2: gb_hcg:
 3: gb_in:
 4: gb_om:
 5: gb_ov:
 6: gb_pat:
 7: gb_ph:
 8: gb_dl:
 9: gb_pr:
 10: gb_ro:
 11: gb_sts:
 12: gb_sy:
 13: gb_un:
 14: gb_vl:
 15: gb_xm:
 16: gb_yt:
 17: gb_zn:
 18: gb_zv:
 19: gb_zx:
 20: gb_zy:
 21: gb_zz:
 22: gb_aa:
 23: gb_ab:
 24: gb_ac:
 25: gb_ad:
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 27: gb_ag:
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 30: gb_ao:
 31: gb_ap:
 32: gb_ar:
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 34: gb_at:
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 45: gb_ba:
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 47: gb_ba:
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 49: gb_ba:
 50: gb_ba:

ALIGNMENTS

RESULT 1
 AX098621 Locus AX098621 Sequence 18 from Patent WO120030.
 DEFINITION Sequence 18 from Patent WO120030.
 ACCESSION AX098621
 VERSION AX098621.1 GR:15537882
 KEYWORDS synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCES 1 Giordano,G., dos Santos,J.P. and Meijean,V.
 AUTHORS TITLE Nucleotide sequences derived from genes coding for trimethylamine
 n-oxide reductase, uses thereof in particular for detecting
 bacteria

JOURNAL Patent: WO 0120030-A 18 22-MAR-2001;
 FEATURES Source
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
 Location/Qualification
 1. 16 /organism="synthetic construct"
 /mol type="unassigned DNA"
 /db Xref="taxon:32630"
 /note="amorce PCR",

ORIGIN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	87.5	16	6	AX098621		AX098621 Sequence
C 2	14	87.5	236	11	DM22G6T	Z50523 D. melanogaster
C 3	14	87.5	594	6	BD163513	BD163513 Novel Pol
C 4	14	87.5	594	6	AX121396	AX121396 Sequence
C 5	14	87.5	641	1	AY325561	AY325561 Unculture
6	14	87.5	641	1	AY325609	AY325609 Unculture
7	14	87.5	643	1	AY209024	AY209024 Unculture
8	14	87.5	643	1	AY209035	AY209035 Unculture
9	14	87.5	644	1	AY209039	AY209039 Unculture
10	14	87.5	644	1	AY325542	AY325542 Unculture
11	14	87.5	645	1	AY552337	AY552337 Unidentif
12	14	87.5	647	1	AY209048	AY209048 Unculture
13	14	87.5	647	1	AY209118	AY209118 Unculture
14	14	87.5	649	1	AY552386	AY552386 Unidentif
15	14	87.5	650	1	AY209084	AY209084 Unculture
16	14	87.5	650	1	AY325570	AY325570 Unculture
17	14	87.5	650	1	AY325522	AY325522 Unculture
18	14	87.5	650	1	AY325562	AY325562 Unculture
19	14	87.5	650	1	AY325585	AY325585 Unculture

RESULT 2
 DM22G6T/c LOCUS DM22G6T

236 bp DNA linear STS 17-APR-1996

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OM nucleic - nucleic search, using bw model

Run on: June 1, 2005, 22:48:55 ; Search time 15.9815 Seconds
(without alignments)

5926.580 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgpyatcttcgtcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 439026 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

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2: geneseqn2001s:*

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4: geneseqn2001as:*

5: geneseqn2001bs:*

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8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	14	87.5	16	4	AAF79957	Aaf79948 Nucleotid
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c 3	14	87.5	594	5	AAB66277	Aaf71276 Corynebac
c 4	14	87.5	741	12	ADJ45730	Aaf79949 Nucleotid
5	14	87.5	741	12	ADJ44921	AdS46046 Bacterial
6	14	87.5	883	13	ADS56043	Aab72908 DNA encod
c 7	14	87.5	1244	13	ADP05004	Aab93061 DNA encod
c 8	14	87.5	1470	11	ABD03667	Aab92727 DNA encod
c 9	14	87.5	1563	11	ABD04037	Aab86655 DNA encod
10	14	87.5	1696	12	ADM47884	Aad28410 Bacillus
c 11	14	87.5	1887	4	AAB19221	Aah19221 Human sec
12	14	87.5	1905	5	AAS79304	Aab79304 DNA encod
c 13	14	87.5	1936	13	ADS56469	AdS56469 Bacterial
14	14	87.5	2130	8	AC31652	Aca31652 Prokaryot
c 15	14	87.5	2268	8	AC31543	Aca31543 Prokaryot
16	14	87.5	2280	8	AC50924	Aca50924 Prokaryot
17	14	87.5	2328	13	ADM45718	Adt45718 Bacterial
18	14	87.5	2358	8	ACAL9185	Aca19185 Prokaryot
c 19	14	87.5	2358	13	ADS46037	AdS46037 Bacterial
c 20	14	87.5	2454	11	ACH97441	Ach97441 Klebsiell

ALIGNMENTS

RESULT 1	ID	AAF79957	standard; DNA; 16 BP.
XX	XX	AAF79957;	
XX	XX	DT 11-JUN-2001 (first entry)	
XX	XX	DE PCR primer used to amplify trimethylamine N-oxide reductase genes	
XX	XX	KW tora gene; trimethylamine N-oxide reductase; flesh degradation; spoilage bacteria; fish; crustacean; PCR primer; ss.	
OS	OS	Synthetic.	
XX	XX	WO200120030-A2.	
PN	PN	WO200120030-A2.	
XX	XX	PD 22-MAR-2001.	
XX	XX	PP 15-SEP-2000; 20000WO-FR002578.	
PR	PR	15-SEP-1999; 99FR-00011543.	
(CNRS)	(CNRS)	CENT NAT RECH SCI.	
PI	PI	Giordano G, Dos Santos J, Mejean V;	
XX	XX	DR WPI; 2001-244822/25.	
XX	XX	Detecting bacteria that cause degradation in fish, for testing freshness, comprises using probes or primers based on the trimethylamine N-oxide reductase system.	
PS	PS	Claim 7; Page 42; 91PP; French.	
XX	XX	PCR primers AAF79951-66 represent PCR primers used to amplify torA and torC genes. TorA and torC are bacterial proteins of the trimethylamine N-oxide reductase system. TorA nucleic acids are used for detecting, in a	

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 4.94154 Seconds
(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-18
Perfect score: 16
Sequence: 1 cb3ayatcstrctrgcc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 50 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/1/ina/PCUTS_COMBO.seq:
6: /cgn2_6/ptodata/1/ina/backfile1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 1	14	87.5	601	4	US-09-049-016-22155	Sequence 22155, A		SEQUENCE 159206,
c 2	14	87.5	601	4	US-09-049-016-159206	Sequence 159206,		SEQUENCE 159206,
c 3	14	87.5	1470	4	US-09-049-016-2271	Sequence 2271, AP		SEQUENCE 2271
c 4	14	87.5	1563	4	US-09-049-016-2441	Sequence 2641, AP		SEQUENCE 2641
c 5	14	87.5	2454	4	US-09-049-019A-3236	Sequence 3236, AP		SEQUENCE 3236
c 6	14	87.5	2503	4	US-09-049-016-277	Sequence 277, AP		SEQUENCE 277
c 7	14	87.5	3687	4	US-09-049-016-611-1	Sequence 1, APPL		SEQUENCE 1
c 8	14	87.5	3846	4	US-09-049-019A-3225	Sequence 3225, AP		SEQUENCE 3225
c 9	14	87.5	18157	4	US-09-049-016-16193	Sequence 16193, A		SEQUENCE 16193
c 10	14	87.5	180121	4	US-09-055-784-1	Sequence 1, APPL		SEQUENCE 1
c 11	14	87.5	180121	4	US-09-053-990A-1	Sequence 1, APPL		SEQUENCE 1
c 12	82.5	82.5	277	4	US-09-053-990C-14892	Sequence 14892, A		SEQUENCE 14892
c 13	82.5	82.5	368	4	US-09-0521-976-30	Sequence 30, APPL		SEQUENCE 30
c 14	82.5	82.5	762	2	US-09-052-251-2	Sequence 2, APPL		SEQUENCE 2
c 15	82.5	82.5	762	4	US-09-0526-852-2	Sequence 2, APPL		SEQUENCE 2
c 16	82.5	82.5	15853	4	US-09-049-016-12121	Sequence 12121, A		SEQUENCE 12121
c 17	82.5	82.5	15853	4	US-09-049-016-16051	Sequence 16051, A		SEQUENCE 16051
c 18	81.2	81.2	263	4	US-09-016-434-1783	Sequence 4863, AP		SEQUENCE 4863
c 19	81.2	81.2	351	4	US-09-0767-4863	Sequence 20144, A		SEQUENCE 20144
c 20	81.2	81.2	351	4	US-09-0767-20145	Sequence 45, APPL		SEQUENCE 45
c 21	81.2	81.2	416	4	US-09-044-598B-45	Sequence 45, APPL		SEQUENCE 45
c 22	81.2	81.2	416	4	US-09-0543-771B-45	Sequence 2, APPL		SEQUENCE 2
c 23	81.2	81.2	440	2	US-08-518-857-2	Sequence 178, APPL		SEQUENCE 178
c 24	81.2	81.2	601	4	US-09-049-016-42148	Sequence 42148, A		SEQUENCE 42148
c 25	81.2	81.2	699	4	US-09-902-540-5926	Sequence 5926, AP		SEQUENCE 5926
c 26	81.2	81.2	700	4	US-09-050-540-185	Sequence 185, APPL		SEQUENCE 185
c 27	81.2	780	3	US-08-990-823-70	Sequence 70, APPL		SEQUENCE 70	

ALIGNMENTS

RESULT 1
US-09-949-016-22155/C
; Sequence 22155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIORITY NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 22155
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-22155
Query Match 87.5%; Score 14; DB 4;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 12; Conservative 4; Mismatches 0;
Indels 0; Gaps 0;
Qy 1 CGGATCCGTCGCC 16
Db 63 CGGATCCGTCGCC 48
RESULT 2
US-09-949-016-159206/C
; Sequence 159206, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 17.0277 Seconds

(without alignments)
 5776.400 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16
 Sequence: 1 cbgayatcstrtggcc 16Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA:*

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 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq;*
 7: /cgn2_6/ptodata/2/pubpna/us08_NEW_PUB.seq;*
 8: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq;*
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16: /cgn2_6/ptodata/2/pubpna/us10E_PUBCOMB.seq;*
17: /cgn2_6/ptodata/2/pubpna/us10F_PUBCOMB.seq;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	87.5	263	9 US-09-923-876-467	Sequence 467, App
2	14	87.5	263	9 US-09-923-876-467	Sequence 467, App
C 3	14	87.5	594	9 US-09-738-626-1312	Sequence 1312, App
C 4	14	87.5	741	17 US-10-369-493-661	Sequence 661, App
C 5	14	87.5	741	17 US-10-260-238-5921	Sequence 5921, App
C 6	14	87.5	911	18 US-10-425-115-42253	Sequence 42253, App
C 7	14	87.5	883	17 US-10-367-493-3117	Sequence 3117, App
8	14	87.5	1696	17 US-10-310-154-302	Sequence 302, App
9	14	87.5	1696	19 US-10-732-923-246	Sequence 246, App
10	14	87.5	1956	17 US-10-367-493-32143	Sequence 32143, App
11	14	87.5	2130	17 US-10-282-122A-19522	Sequence 19522, App

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	14	87.5	2358	17 US-10-369-493-24467	Sequence 24467, App
4	14	87.5	2547	17 US-10-369-493-24476	Sequence 24476, App
5	14	87.5	3687	9 US-09-891-641-1	Sequence 1, Appli
6	14	87.5	3687	17 US-10-369-493-47029	Sequence 47029, App
7	14	87.5	3687	17 US-10-602-747A-1	Sequence 1, Appli
8	14	87.5	3687	17 US-10-282-122A-22928	Sequence 22928, App
9	14	87.5	3744	9 US-09-815-542-9443	Sequence 9443, App
10	14	87.5	3744	9 US-09-738-626-1314	Sequence 1314, App
11	14	87.5	3744	17 US-10-282-122A-39793	Sequence 39793, App
12	14	87.5	3744	17 US-10-240-689-39	Sequence 1, Appli
13	14	87.5	3744	19 US-10-925-357-1	Sequence 1, Appli
14	14	87.5	3744	17 US-10-329-670-1	Sequence 1, Appli
15	14	87.5	3744	18 US-10-158-865-1	Sequence 1, Appli
16	14	87.5	3744	19 US-10-497-078-125	Sequence 1, Appli
17	14	87.5	3744	13 US-10-027-632-16473	Sequence 1, Appli
18	14	87.5	36401	19 US-10-925-191-1	Sequence 1, Appli
19	14	87.5	1830121	17 US-10-282-122A-22928	Sequence 22928, App
20	14	87.5	1830121	18 US-10-329-670-1	Sequence 9443, App
21	14	87.5	11275	16 US-10-240-689-39	Sequence 1, Appli
22	14	87.5	3687	17 US-10-925-357-1	Sequence 1, Appli
23	14	87.5	3744	9 US-09-738-626-1314	Sequence 1314, App
24	14	87.5	3744	17 US-10-282-122A-39793	Sequence 39793, App
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26	14	87.5	3744	19 US-10-925-357-1	Sequence 1, Appli
27	14	87.5	36401	19 US-10-925-191-1	Sequence 1, Appli
28	14	87.5	1830121	17 US-10-282-122A-22928	Sequence 22928, App
29	14	87.5	1830121	18 US-10-329-670-1	Sequence 9443, App
30	14	87.5	3309400	9 US-09-738-626-1	Sequence 1314, App
31	14	87.5	653	19 US-10-497-078-125	Sequence 1, Appli
32	14	82.5	712	13 US-10-027-632-16473	Sequence 1, Appli
33	13.2	82.5	762	15 US-10-316-761-2	Sequence 1, Appli
34	13.2	82.5	762	15 US-10-027-632-264695	Sequence 264695, App
35	13.2	82.5	3137	13 US-10-027-632-264695	Sequence 264695, App
36	13.2	82.5	3137	17 US-10-027-632-264695	Sequence 264695, App
37	13	81.2	25	19 US-10-719-900-37229	Sequence 1, Appli
38	13	81.2	25	19 US-10-719-900-185408	Sequence 1, Appli
39	13	81.2	47	14 US-10-013-173-16	Sequence 16, App
40	13	81.2	47	15 US-10-150-762-16	Sequence 16, App
41	13	81.2	47	15 US-10-244-821-16	Sequence 16, App
C 43	13	81.2	141	18 US-10-425-115-95266	Sequence 95266, App
44	13	81.2	192	15 US-10-156-761-5179	Sequence 5179, App
45	13	81.2	263	17 US-10-305-720-178	Sequence 178, App
46	13	81.2	302	18 US-10-425-115-12070	Sequence 12070, App
C 48	13	81.2	359	9 US-09-917-800A-691	Sequence 691, App
49	13	81.2	398	16 US-10-029-386-14441	Sequence 14441, App
50	13	81.2	401	9 US-09-64-761-32357	Sequence 32357, App
		414	18	US-10-425-115-87116	Sequence 87116, App

ALIGNMENTS

RESULT 1	US-09-923-876-467	Application US/0923876
	; Patent No. US20020013958A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Laljude, Raghunath V.	
	; ATTORNEY: Kamigaki, Laura Y. (Ito)	
	; PRIORITY: Sherman, Bradley K.	
	; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING	
	; FILE REFERENCE: PL-0012-1 CON	
	; CURRENT APPLICATION NUMBER: US/09/923, 876	
	; CURRENT FILING DATE: 2001-08-06	
	; PRIOR APPLICATION NUMBER: 09/298, 329	
	; SOFTWARE: PERL Program	
	; SEQ ID NO: 467	
	; LENGTH: 263	
	; TYPE: DNA	
	; ORGANISM: Zea mays	
	; FEATURE:	
	; NAME/KEY: misc feature	
	; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156983H1	
	; US-09-923-876-467	

US-09-923-876-467	Application US/0923876
	; Patent No. US20020013958A1
	; GENERAL INFORMATION:
	; APPLICANT: Laljude, Raghunath V.
	; ATTORNEY: Kamigaki, Laura Y. (Ito)
	; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
	; FILE REFERENCE: PL-0012-1 CON
	; CURRENT APPLICATION NUMBER: US/09/923, 876
	; CURRENT FILING DATE: 2001-08-06
	; PRIOR APPLICATION NUMBER: 09/298, 329
	; SOFTWARE: PERL Program
	; SEQ ID NO: 467
	; LENGTH: 263
	; TYPE: DNA
	; ORGANISM: Zea mays
	; FEATURE:
	; NAME/KEY: misc feature
	; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156983H1
	; US-09-923-876-467

US-09-923-876-467	Application US/0923876
	; Patent No. US20020013958A1
	; GENERAL INFORMATION:
	; APPLICANT: Laljude, Raghunath V.
	; ATTORNEY: Kamigaki, Laura Y. (Ito)
	; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
	; FILE REFERENCE: PL-0012-1 CON
	; CURRENT APPLICATION NUMBER: US/09/923, 876
	; CURRENT FILING DATE: 2001-08-06
	; PRIOR APPLICATION NUMBER: 09/298, 329
	; SOFTWARE: PERL Program
	; SEQ ID NO: 467
	; LENGTH: 263
	; TYPE: DNA
	; ORGANISM: Zea mays
	; FEATURE:
	; NAME/KEY: misc feature
	; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156983H1
	; US-09-923-876-467

US-09-923-876-467	Application US/0923876
	; Patent No. US20020013958A1
	; GENERAL INFORMATION:
	; APPLICANT: Laljude, Raghunath V.
	; ATTORNEY: Kamigaki, Laura Y. (Ito)
	; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
	; FILE REFERENCE: PL-0012-1 CON
	; CURRENT APPLICATION NUMBER: US/09/923, 876
	; CURRENT FILING DATE: 2001-08-06
	; PRIOR APPLICATION NUMBER: 09/298, 329
	; SOFTWARE: PERL Program
	; SEQ ID NO: 467
	; LENGTH: 263
	; TYPE: DNA
	; ORGANISM: Zea mays
	; FEATURE:
	; NAME/KEY: misc feature
	; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156983H1
	; US-09-923-876-467

Result	No.	Score	Query Match	Length	DB ID	Description	FEATURES
c	1	14	87.5	188	9 CG733285	CG733285 1119155C1 A2868010	/organism="Zea mays"
c	2	14	87.5	219	8 A2868010	A2857279 2M0162603	/mol_type="genomic DNA"
c	3	14	87.5	237	8 A2857279	A1881564 606070610	/cultivar="mixed background"
c	4	14	87.5	259	8 A1881564	A2755055 cg07e04.f	/db_xref="taxon:4577"
c	5	14	87.5	328	8 A2755055	W87131 mf5f03.r1	/tissue_type="leaf"
c	6	14	87.5	363	7 W87131	BG837422 2m10_07a1	/dev_stage="adult"
c	7	14	87.5	365	4 BG837422	W11810 mb30a06_r1	/lab_host="DH10B"
c	8	14	87.5	381	7 W1110	CD783767 EST6555128	/clone_lib="1119 - RescueMu Grid AA"
c	9	14	87.5	391	6 CD783767	BY298653 BY298653	/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
c	10	14	87.5	408	5 CD091125	CD091125 MCL-0085G	RescueMu is a 4.9 kb, modified maize mu transposon
c	11	14	87.5	423	6 CD091125	BP339064 BP339064	designed to allow plasmid rescue from total genomic DNA.
c	12	14	87.5	459	8 BH240839	CR205324 Reverse S	Mu elements insert preferentially into transposon units. For more information on RescueMu, go to the web
c	13	14	87.5	484	5 BU266837	CB536706 771746 MA	
c	14	14	87.5	492	1 AB914387	CD780356 EST651717	
c	15	14	87.5	513	8 BA7814	CD785404 EST656765	
c	16	14	87.5	529	8 AQ434937	C0531075 3530_1-20	
c	17	14	87.5	537	6 CD793456	C0531075 3530_1-19	
c	18	14	87.5	550	5 BP339064	C0530140 3530_1-19	
c	19	14	87.5	570	9 CR205324		
c	20	14	87.5	578	6 CB536706		
c	21	14	87.5	586	6 CD780356		
c	22	14	87.5	589	6 CD785404		
c	23	14	87.5	594	7 C0531075		
c	24	14	87.5	603	7 C0530140		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
CG733285
LOCUS 1119155C1.y1 1119 - Rescuemu Grid AA Zea mays genomic sequence.
DEFINITION survey sequence.
ACCESSION CG733285
VERSION CG733285.1 GI:37775777
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidea; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 188)
AUTHORS Walbot, V.
TITLE Maize Genomic Sequences found using engineered Rescuemu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Pline: 1119155 row: 6
Class: transposon-tagged.
Location/Qualifiers Location/Qualifiers
Source

ALIGNMENTS

Title: US-10-088-117A-18
Perfect score: 16
Sequence: 1 cbgagatcstrctgcc 16

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :	EST.*
1:	gb_est1:*
2:	gb_est2:*
3:	gb_htc:*
4:	gb_est3:*
5:	gb_est4:*
6:	gb_est5:*
7:	gb_est6:*
8:	gb_gss1:*
9:	gb_gss2:*

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Om nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds

(without alignments)
 6151.841 Million cell updates/sec.

Title: US-10-088-117A-19

Perfect score: 20

Sequence: 1 ggmgaytaytcbacmgygc 20

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 50 summaries

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1: gb_ba:*

2: gb_hrg:*

3: gb_in:*

4: gb_on:*

5: gb_ov:*

6: gb_dat:*

7: gb_bh:*

8: gb_dl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	17.2	86.0	20	6	AX098622	AX098622 Sequence
2	17.2	86.0	1998	6	AR387097	AR387097 Sequence
3	17.2	86.0	2385	6	AR387009	AR387009 Sequence
4	17.2	86.0	2475	6	AX098610	AX098610 Sequence
5	17.2	86.0	2486	6	AX098605	AX098605 Sequence
6	17.2	86.0	2487	6	AX098614	AX098614 Sequence
7	17.2	86.0	2487	6	AX098606	AX098606 Sequence
8	17.2	86.0	2490	1	SPU5974	AJ005974 Shewaneill
9	17.2	86.0	2523	6	AX098609	AX098609 Sequence
10	17.2	86.0	2540	1	RCDSTNORG	X950407 R capsulatus
11	17.2	86.0	2544	6	AX098612	AX098612 Sequence
c 12	17.2	86.0	3235	1	AF134121	AF134121 Helicobac
13	17.2	86.0	4680	1	ECTOR	T3388 E. coli gene
14	17.2	86.0	5637	1	RCU49506	U49556 Rhodobacter
15	17.2	86.0	6915	1	SMA6085	AJ005985 Shewaneill
16	17.2	86.0	7990	1	AF016236	AF016236 Rhodobact
c 17	17.2	86.0	10726	1	AE015567	AE015567 Shewaneill
18	17.2	86.0	13067	1	AB015128	D90737 Bacteri
19	17.2	86.0	18252	1	D90737	D90737 Bacteri

D90736 Escherichia
 AE008869 Salmonell
 Continuation (11 o
 AC051613 Mus muscu
 AL627281 Salmonell
 AC090533 Mus muscu
 AE016981 Shigella
 AE016847 Salmonell
 AE016758 Escherich
 AE017147 Helicobac
 AX098615 Sequence
 AE004270 Vibrio ch
 CQ442053 Sequence
 M34827 E. coli biot
 AB015366 Shigella
 AB006216 Pasteurel
 AE005582 Escherich
 AE005293 Escherich
 AE008878 Salmonell
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 AC073552 Homo sapi
 AC148336 Macaca mu
 AC007249 Homo sapi
 U00039 E. coli chr
 AL622780 Salmonell
 AP002365 Escherich
 AB016392 Shigella
 AP005077 Vibrio pa
 AE016846 Salmonell
 AB016768 Escherich
 AP002254 Escherich

ALIGNMENTS

20 bp DNA linear PAT 02-APR-2001
 AX098622 Sequence 173938 2 AC148336
 LOCUS AX098622 Sequence 173938 2 AC148336
 DEFINITION Sequence 19 from Patent WO0120030.
 AC007249 Homo sapi
 AX098622 Sequence AX098622 9 AC007249 Homo sapi
 VERSION AX098622.1 GI:13537883
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 1 Giordano,G., dos Santos,J.P. and Mejean,V.
 REFERENCE
 AUTHORS
 TITLE Nucleotide sequences derived from genes coding for trimethylamine
 n-oxide reductase, uses thereof in particular for detecting
 bacteria

PATENT: WO 0120030-A 19 22-MAR-2001:
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
 Location/Qualifiers
 1. -20
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_Xref="taxon:12630"
 /note="amorce PCR"
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 Query Match 86.0% Score 17.2%; DB 6;
 Best Local Similarity 100.0%; Pred. No. 1e-03;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 GGMGAYTAYTCBAAGGGYGC 20
 Db 1 GGMGAYTAYTCBAAGGGYGC 20
 RESULT 2 AR387097/c
 LOCUS AR387097
 1998 bp DNA linear PAT 18-DEC-2003

2: geneseqn2009bs:
 3: geneseqn2009bs:
 4: geneseqn2001ab:**
 5: geneseqn2001ab:**
 6: geneseqn2002ab:**
 7: geneseqn2002ab:**
 8: geneseqn2003ab:**
 9: geneseqn2003ab:**
 10: geneseqn2003cb:**
 11: geneseqn2003ds:**
 12: geneseqn2004as:**
 13: geneseqn2004bs:**

SUMMARIES

result	No.	Score	Query	Match	Length	DB	ID	Description
	1	17.2	86.0	20	4	AAFP79958	AafP79958 PCR prime	
	2	17.2	86.0	1998	11	ACH98031	Ach98031 Klebsiella	
c	3	17.2	86.0	2385	11	ACH97943	Ach97943 Klebsiella	
	4	17.2	86.0	2475	4	AAFP79948	AafP79948 Nucleotid	
	5	17.2	86.0	2486	4	AAFP79944	AafP79944 Nucleotid	
	6	17.2	86.0	2487	4	AAFP79945	AafP79945 Nucleotid	
	7	17.2	86.0	2487	4	AAFP79943	AafP79943 Nucleotid	
	8	17.2	86.0	2523	4	AAFP79947	AafP79947 Nucleotid	
	9	17.2	86.0	2554	4	AAFP79949	AafP79949 Nucleotid	
	10	17.2	86.0	2557	13	ADSG6046	Adg6046 Bacterial	
	11	17.2	86.0	11257	6	AAH43717	Aah43717 E. coli 9	
	12	16.4	82.0	21	4	AAFP79951	AafP79951 PCR prime	
	13	16.2	81.0	408	6	ABN15673	Abn15673 Human ORF	
	14	16	80.0	1455	5	AAS86797	Aas86797 DNA encod	
c	15	16	80.0	2220	13	ADP48846	Adp48846 Bacterial	
	16	15.6	78.0	780	11	ABD01207	Abd01207 Klebsiella	
	17	15.6	78.0	2120	13	ADSS8851	Adss8851 Bacterial	
	18	15.6	78.0	2556	8	ACAA38838	Aca38838 Prokaryot	
	19	15.6	78.0	2637	12	ADU03795	Adu03795 DNA encod	
	20	15.6	78.0	2742	13	ADPR5388	Adpr5388 Aspergillus	

WO2000120030

ALIGNMENTS

RESULT 1
 AAF79938
 ID AAF79938 standard; DNA; 20 BP.
 XK
 AC
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DB PCR primer used to amplify trimethylamine N-oxide reductase genes.
 XK tora gene; trimethylamine N-oxide reductase; flesh degradation;
 KW spoiling bacteria; fish; crustacean; PCR primer; ss.

PCR primers used to amplify torA and torC genes. TIR and TOR are bacterial proteins of the trimethylamine N-oxide reductase system. TIR nucleic acids are used for detecting in a PCR assay comprising using probes or primers based on the trimethylamine N-oxide reductase system.

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005; 08:20:11 ; Search time 6.17692 Seconds (without alignments)

5298.032 Million cell updates/sec

Title: US-10-088-117a-19

Perfect score: 20

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Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

RESULT 1
US-09-489-039A-3826/c
; Sequence 3826, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709_2004001
; CURRENT FILING DATE: 2000-01-27
; PRIORITY NUMBER: US/09/489,039A
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3826
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-3826

Query Match 86.0%; Score 17.2; DB 4; Length 1998;
Best Local Similarity 70.0%; Pred. No. 9.6;
Matches 14; Conservative 6; Mis matches 0;
Indels 0; Gaps 0;

Qy 1 GGMGAYTAYTCBACGGYGC 20
Db 1770 GGCGATTACTCCACGGGC 1751

RESULT 2
US-09-489-039A-3738
; Sequence 3738, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709_2004001
; CURRENT FILING NUMBER: US/09/489,039A
; PRIORITY NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3738
; LENGTH: 2385

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c 2	17.2	86.0	2385	4 US-09-489-039A-3738	Sequence 3738, Ap
c 3	15.6	78.0	780	4 US-09-489-039A-6982	Sequence 6982, Ap
c 4	15.6	78.0	2637	4 US-09-540-036-1481	Sequence 1481, Ap
c 5	15.6	78.0	23210	4 US-09-596-002-17	Sequence 17, Appl
c 6	14.4	72.0	303	4 US-09-513-999C-11097	Sequence 11097, A
c 7	14.4	72.0	312	3 US-09-060-756-506	Sequence 506, App
c 8	14.4	72.0	312	4 US-09-670-314-506	Sequence 506, App
c 9	14.4	72.0	459	4 US-09-489-039A-6694	Sequence 6694, Ap
c 10	14.4	72.0	1752	4 US-09-489-039A-6747	Sequence 6747, Ap
c 11	14.4	72.0	82125	4 US-09-949-016-1517	Sequence 13517, A
c 12	14.4	72.0	82125	4 US-09-949-016-13518	Sequence 13518, A
c 13	14.4	72.0	15030	4 US-09-149-016-14896	Sequence 14896, A
c 14	14.4	72.0	1230230	4 US-09-438-185A-1	Sequence 1, Appl
c 15	14.4	72.0	251682	4 US-09-949-016-17296	Sequence 17296, A
c 16	14.4	72.0	4403765	3 US-09-103-840A-2	Sequence 2, Appl
c 17	14.4	72.0	4411529	3 US-09-103-840A-1	Sequence 1, Appl
c 18	14.2	71.0	2294	4 US-09-270-767-10469	Sequence 10469, A
c 19	14.2	71.0	130025	4 US-09-198-452A-1	Sequence 1, Appl
c 20	14.2	71.0	1230230	4 US-09-438-185A-1	Sequence 1, Appl
c 21	14	70.0	93	3 US-08-952-79-269	Sequence 269, App
c 22	14	70.0	93	4 US-09-849-028-269	Sequence 269, App
c 23	14	70.0	93	5 PCT-US96-0455A-269	Sequence 269, App
c 24	14	70.0	281	4 US-09-513-999C-12276	Sequence 12276, A
c 25	14	70.0	458	4 US-09-252-991A-8183	Sequence 8183, Ap
c 26	14	70.0	597	4 US-09-949-016-20773	Sequence 20773, A
c 27	14	70.0	601	4 US-09-949-016-20774	Sequence 20774, A
c 28	14	70.0	601	4 US-09-949-016-96203	Sequence 96203, A
c 29	14	70.0	601	4 US-09-949-016-96204	Sequence 96204, A
c 30	14	70.0	601	4 US-10-043-038-2	Sequence 2, Appl
c 31	14	70.0	954	4 US-10-043-038-2	Sequence 5955, Ap
c 32	14	70.0	1101	4 US-09-252-991A-5955	Sequence 123, App
c 33	14	70.0	1287	4 US-09-489-039A-123	Sequence 123, App
c 34	14	70.0	1368	4 US-09-190-514-7420	Sequence 1213, App
c 35	14	70.0	1383	4 US-09-252-991A-1213	Sequence 1213, App
c 36	14	70.0	1503	4 US-09-252-991A-7970	Sequence 7970, Ap
c 37	14	70.0	1773	4 US-09-489-039A-241	Sequence 241, App
c 38	14	70.0	2262	4 US-09-252-991A-1353	Sequence 1353, App
c 39	14	70.0	2418	4 US-09-252-991A-1251	Sequence 1251, App
c 40	14	70.0	2559	3 US-09-029-267-19	Sequence 19, Appl
c 41	14	70.0	2659	3 US-09-029-267-19	Sequence 19, Appl
c 42	14	70.0	3840	4 US-09-489-039A-6431	Sequence 6431, Ap
c 43	14	70.0	4171	4 US-09-167-422-3	Sequence 3, Appl
c 44	14	70.0	7317	4 US-09-902-540-715	Sequence 715, App
c 45	14	70.0	8157	1 US-08-358-160-65	Sequence 65, App
c 46	14	70.0	8578	4 US-09-190-514-871	Sequence 66, App
c 47	14	70.0	8584	1 US-08-358-160-66	Sequence 70, App
c 48	14	70.0	8590	1 US-08-358-160-70	Sequence 138, App
c 49	14	70.0	35961	4 US-08-311-731A-138	Sequence 138, App

ALIGNMENTS

12	15.2	76.0	1883	18	US-10-357-930-23456
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14	15.2	76.0	2448	17	US-10-369-493-24560
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c	16	75.0	655	18	US-10-653-047-169
c	17	75.0	980	18	US-10-767-795-3190
c	18	75.0	1435	18	US-10-767-795-507
c	19	75.0	3291	17	US-10-263-929-50
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c	21	14.8	0	330940	9
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c	23	14.6	73.0	347	17
c	24	14.6	73.0	359	18
c	25	14.6	73.0	523	18
c	26	14.6	73.0	523	18
c	27	14.6	73.0	657	18
c	28	14.6	73.0	668	18
c	29	14.6	73.0	767	18
c	30	14.6	73.0	776	13
c	31	14.6	73.0	776	17
c	32	14.6	73.0	782	18
c	33	14.6	73.0	823	13
c	34	14.6	73.0	823	13
c	35	14.6	73.0	823	17
c	36	14.6	73.0	823	17
c	37	14.6	73.0	879	18
c	38	14.6	73.0	967	18
c	39	14.6	73.0	988	17
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c	42	14.6	73.0	2102	18
c	43	14.6	73.0	3006	19
c	44	14.6	73.0	3459	18
c	45	14.6	73.0	4299	19
c	46	14.6	73.0	248436	13
c	47	14.4	72.0	25	19
c	48	14.4	72.0	300	18
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Perfect score:	20				
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Scoring table:	IDENTITY_NUC				
	Gapop 10_0 , Gapext 1.0				
Searched:	5706582 seqs, 303711274 residues				
Total number of hits satisfying chosen parameters:	11413164				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
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Published Applications_NA*					
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9:	/cgn2_6/ptodata/2/pubnra/us09A_pubcomb.seq*				
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ALIGNMENTS													
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13:	/cgn2_6/_podata/2/_pubpna/_US10A_PUBCOMB.seq;*												
14:	/cgn2_6/_podata/2/_pubpna/_US10B_PUBCOMB.seq;*												
15:	/cgn2_6/_podata/2/_pubpna/_US10C_PUBCOMB.seq;*												
16:	/cgn2_6/_podata/2/_pubpna/_US10D_PUBCOMB.seq;*												
17:	/cgn2_6/_podata/2/_pubpna/_US10E_PUBCOMB.seq;*												
18:	/cgn2_6/_podata/2/_pubpna/_US10F_PUBCOMB.seq;*												
19:	/cgn2_6/_podata/2/_pubpna/_US10_NNEW_PUB.seq;*												
20:	/cgn2_6/_podata/2/_pubpna/_US11_NNEW_PUB.seq;*												
21:	/cgn2_6/_podata/2/_pubpna/_US60_NNEW_PUB.seq;*												
22:	/cgn2_6/_podata/2/_pubpna/_US60_PUBCOMB.seq;*												
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.													
SUMMARIES													
result	Query	Match	Length	DB ID	Description								
No.	No.	Score	Match	Length	DB ID								
1.	17.2	86.0	2547	17	US-10-669-493-24476	Sequence 24476, A	SEQ ID NO: 24476						
2	17.2	86.0	11275	16	US-10-210-683-39	Sequence 39, Appl	LENGTH: 2547						
3	16	80.0	2220	17	US-10-669-493-47884	Sequence 47284, A	TYPE: DNA						
4	15.6	78.0	398	17	US-10-242-555A-21879	Sequence 21879, A	ORGANISM: Escherichia coli						
5	15.6	78.0	398	17	US-10-085-783A-21879	Sequence 21879, A	US-10-669-493-24476						
6	15.6	78.0	2120	17	US-10-669-493-34525	Sequence 34525, A							
7	15.6	78.0	2556	17	US-10-282-122A-26708	Sequence 26708, A							
8	15.6	78.0	3201	18	US-10-037-963-54573	Sequence 54673, A							
c	9	15.6	78.0	23210	17	US-10-072-707-17	Sequence 17, Appl	Query Match 86.0%; Best Local Similarity 70.0%; Pred. No. 20; Matches 14; Conservative 6; Mismatched 1					
c	10	15.6	78.0	27314	18	US-10-297-465A-1	Sequence 1, Appl						
c	11	15.2	1883	18	US-10-337-930-23102	Sequence 23102, A							

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	C49840 C49840 Yuji					
OM nucleic - nucleic search, using sw model	AU207172 AU207172					
Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds	BU119459 BU119459					
(without alignments)	AQ555032 RPOT-11-4					
5660.438 Million cell updates/sec	CC993846 ZUDI64TV					
Title: US-10-088-117a-19	BU104489 BU104489					
Perfect score: 20	CB402008 CB402008					
Sequence: 1 ggmgaytaytcbacmgygc 20	BJ109482 BJ109482					
Scoring table: IDENTITY NUC	CB399218 GSTR218C					
Gapop 10.0 , Gapext 1.0	CO112335 GR EB004					
Searched: 34239544 seqs, 19032134700 residues	BJ104229 BJ104229					
Total number of hits satisfying chosen parameters:	BZ570305 mesh2_1309					
Minimum DB seq length: 0	BU112730 BU112730					
Maximum DB seq length: 2000000000	BJ762214 BJ762214					
Post-processing: Minimum Match 0%	CN145218 WOUND1_27					
Maximum Match 100%	CC798790 ZMMBBB045					
Listing first 50 summaries	BI489244 603021456					
Database :	ALIGMENTS					
EST:*	RESULT 1					
1: gb_est1:*	BG456299 /c					
2: gb_est2:*	BG456299					
3: gb_hnc:*	NFO76D01PL1F028 Phosphate starved leaf Medicago truncatula cDNA					
4: gb_est3:*	DEFINITION NFO76D01PL1F028 Phosphate starved leaf Medicago truncatula cDNA					
5: gb_est4:*	CL41049 ZMMBBB05					
6: gb_est5:*	CC622684 OGUBJB25TV					
7: gb_est6:*	CG656299					
8: gb_gss1:*	CN145218					
9: gb_gss2:*	CK775307 966431 MA					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	CG875316 CL263736					
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c 1	17.2	86.0	684	4	BG456299	BG456299 NF076D03P
c 2	17.2	86.0	690	9	CL658599	PR10131d BH370263 AG-ND-105
c 3	17.2	86.0	715	8	CB088161	hn6104_9 CB088161 AG-ND-137
c 4	17.2	86.0	716	6	CB402590	AG-ND-137 CL669134 PR10139c
c 5	17.2	86.0	773	8	CL669134	BH388945 AG-ND-137
c 6	17.2	86.0	794	8	BP182266	BH388945 AG-ND-137
c 7	17.2	86.0	799	8	BP182266	CL671059 PRI0163d
c 8	17.2	86.0	812	9	BP182266	AW226349 ST81D01_P
c 9	16.4	82.0	385	2	CM536619	CW536619 OP_Ba003
c 10	16	80.0	531	9	CM531185	CW531185 OP_Ba003
c 11	16	80.0	795	9	CM539148	CW539148 OP_Ba005
c 12	16	80.0	798	9	BP182266	BP182266 6016018
c 13	16	80.0	846	2	CM528614	CW528614 OP_Ba004
c 14	16	80.0	853	9	CM505482	CW505482 OP_Ba000
c 15	16	80.0	902	9	CM505482	CM505482 OP_Ba000
c 16	16	80.0	1088	9	CNS06XDO	AL419607 end of
c 17	15.6	78.0	349	2	AU225724	AU225724
c 18	15.6	78.0	360	6	C48572	C48572 Yuji
c 19	15.6	78.0	360	6	C50548	C50548 Yuji
c 20	15.6	78.0	360	7	D75946	CBLK112B9P
c 21	15.6	78.0	360	7	T00584	T00584 WES701305_E
c 22	15.6	78.0	374	6	C48425	C48425 Yuji
c 23	15.6	78.0	376	1	AV194216	AV194216
c 24	15.6	78.0	378	1	AV194014	AV194014

RESULT 1
BG456299 /c
LOCUS BG456299
DEFINITION NFO76D01PL1F028 Phosphate starved leaf Medicago truncatula cDNA
ACCESSION CL41049 ZMMBBB05
VERSION CC622684 OGUBJB25TV
KEYWORDS CK775307
SOURCE EST.
ORGANISM Medicago truncatula (barrel medic)
MEDICAGO truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicots;
rosids; eurosids I; Fabales; Papilionoideae; Trifoliaceae; Medicago.
1 (bases 1 to 684)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Waller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Unpublished
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mharrison@noble.org
Insert Length: 684 Std Error: 0.00
Plate: 076 row: D column: 03
Seq primer: TCACACGGAAACGTATGAC.
FEATURES Location/Qualifiers
Source /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:33800"
/clone="NF076D03PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_id="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds
(without alignments)

6151.841 Million cell updates/sec

Title: US-10-088-117A-20
Perfect score: 20

Sequence: 1 twygarcgaaacgatmtcga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100§

Listing first 50 summaries

Database : GenBank:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:

RESULT 1
AX098623
LOCUS Sequence 20 from Patent WO120030.

DEFINITION Sequence 20 from Patent WO120030.

ACCESSION AX098623.1

VERSION GI:13537884

KEYWORDS synthetic construct

ORGANISM synthetic construct

OTHER SEQUENCES; ARTIFICIAL SEQUENCES.

REFERENCE 1 Giordano,G., dos Santos,J.-P. and Mejian,V.

AUTHORS Nucleotide sequences derived from genes coding for trimethylamine

TITLE n-oxide reductase, uses thereof in particular for detecting

bacteria

Patent: WO 0120030 A 20 22-MAR-2001;

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

JOURNAL 1. 20

FEATURES /organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN Query Match Similarity 88.0%; Score 17.6; DB 6; Length 20;

Source Best Local Similarity 88.0%; Pred No 87; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTYGARGCGYAAAGATMTCGA 20

Db 1 TTYGARGCGYAAAGATMTCGA 20

RESULT 2 RSU25037

LOCUS RSU25037

2292 bp

DNA linear

BCT 16-APR-1998

ALIGNMENTS

20	17.6	88.0	13067	1	AB015128
21	17.6	88.0	18252	1	D90737
22	17.6	88.0	19650	1	D90736
c	23	17.6	22418	1	AB008878
c	24	17.6	110000	1	U000610
c	25	17.6	214911	2	AC010537
c	26	17.6	245050	1	AL622280
c	27	17.6	292504	1	AB016981
c	28	17.6	300350	1	AP006574
c	29	17.6	300592	1	AB016846
c	30	17.6	301276	1	AB016758
c	31	17.6	327773	1	AP002554
c	32	16.6	13013	1	AB008592
c	33	16.6	35909	3	LMFL3856
c	34	16.6	110000	1	AE000516_15
c	35	16.6	299450	1	BX248338
c	36	16.6	311281	1	AB016859
c	37	16.6	348264	1	BX842576
c	38	16.4	2501	8	AY260969
c	39	16	174	6	CQ604041
c	40	16	825	6	AK413746
c	41	16	825	6	AK415759
c	42	16	800	1989	CQ647060
c	43	16	800	1992	6
c	44	16	800	2099	6
c	45	16	800	2544	6
c	46	16	800	3558	6
c	47	16	800	4122	6
c	48	16	800	5397	6
c	49	16	800	10362	1
c	50	16	800	10715	1
c	51	16	10715	1	AB006216

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	17.6	88.0	20	6	AX098623	Sequence U025037 Rhodobacter
2	17.6	88.0	2292	1	RSU25037	Sequence AX098610
3	17.6	88.0	2475	6	AX098610	Sequence AX098605
4	17.6	88.0	2486	6	AX098605	Sequence AX098604
5	17.6	88.0	2487	6	AX098606	Sequence AX098606
6	17.6	88.0	2487	6	SPU5974	Sequence AJ0105974 Shewanell
7	17.6	88.0	2490	1	X954609	Sequence AX098609
8	17.6	88.0	2523	6	AK09609	Sequence X954612 Rhodobacter
9	17.6	88.0	2540	1	RCDSN09G	Sequence L46851 Rhodobacter
10	17.6	88.0	2544	6	AX098612	Sequence D38634 Rhodobacter
11	17.6	88.0	2750	1	RCAD5RA	Sequence X73888 E.coli gene
12	17.6	88.0	3316	1	RCADMS	Sequence RCT049506
13	17.6	88.0	4680	1	ECTOR	Sequence AF016236 Rhodobacter
14	17.6	88.0	5637	1	Db	Sequence AE015567 Shewanell
15	17.6	88.0	6915	1	SMK6085	Sequence AE005293 Escherich
16	17.6	88.0	7990	1	Qy	Sequence AE002060 Deinococc
17	17.6	88.0	10726	1	RSU25037	Sequence
18	17.6	88.0	11289	1	LOCUS	
19	17.6	88.0	11378	1		

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-20

Perfect score: 20

Sequence: 1 twygarcgaaacgymtcga 20

Scoring table: IDENTITY_NUC

Gapop: 10.0 , Gapext: 1.0

Searched: 439026 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

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3: geneseqn2000s:
4: geneseqn2000as:
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6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2002as:
9: geneseqn2002bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	17.6	AATP79959	20	4	AATP79959	AatP79959 PCR prime
c 2	17.6	ABQ32142	88.0	812	6	Abq32142 Oligonucleic acid
c 3	17.6	ABQ32143	88.0	812	6	Abq32143 Oligonucleic acid
c 4	17.6	ABQ56937	88.0	2475	4	Abq56937 Listeria
c 5	17.6	ABQ67924	88.0	2486	4	Abq67924 Listeria
c 6	17.6	ABQ67945	88.0	2487	4	Abq67945 Mycobacteria
c 7	17.6	ABQ71748	88.0	2487	4	Abq71748 Streptococcus
c 8	17.6	ABQ80522	88.0	2523	4	Abq80522 Listeria
c 9	17.6	ABQ80569	88.0	2544	4	Abq80569 ABN58052
c 10	17.6	ABQ80572	88.0	2547	13	Abq80572 ABN58052
c 11	17.6	ABQ80573	88.0	2853	5	Abq80573 ABN58052
c 12	17.6	ABQ80574	88.0	2853	5	Abq80574 ABN58052
c 13	17.6	ABQ80575	88.0	2853	5	Abq80575 ABN58052
c 14	17.6	ABQ80576	88.0	2853	5	Abq80576 ABN58052
c 15	17.6	ABQ80577	88.0	11275	6	Abq80577 ABN58052
c 16	16.6	ABQ80578	83.0	4689	8	Abq80578 ABN58052
c 17	16.6	ABQ80579	83.0	110000	4	Abq80579 ABN58052
c 18	16.6	ABQ80580	83.0	110000	4	Abq80580 ABN58052
c 19	16.4	ABQ80581	82.0	1520	6	Abq80581 ABN58052
c 20	16.4	ABQ80582	82.0	1520	6	Abq80582 ABN58052

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	17.6	AATP79959	20	4	AATP79959	AatP79959 PCR prime
c 2	17.6	ABQ32142	88.0	812	6	Abq32142 Oligonucleic acid
c 3	17.6	ABQ32143	88.0	812	6	Abq32143 Oligonucleic acid
c 4	17.6	ABQ56937	88.0	2475	4	Abq56937 Listeria
c 5	17.6	ABQ67924	88.0	2486	4	Abq67924 Listeria
c 6	17.6	ABQ67945	88.0	2487	4	Abq67945 Mycobacteria
c 7	17.6	ABQ71748	88.0	2487	4	Abq71748 Streptococcus
c 8	17.6	ABQ80522	88.0	2523	4	Abq80522 Listeria
c 9	17.6	ABQ80569	88.0	2544	4	Abq80569 ABN58052
c 10	17.6	ABQ80572	88.0	2547	13	Abq80572 ABN58052
c 11	17.6	ABQ80573	88.0	2853	5	Abq80573 ABN58052
c 12	17.6	ABQ80574	88.0	2853	5	Abq80574 ABN58052
c 13	17.6	ABQ80575	88.0	2853	5	Abq80575 ABN58052
c 14	17.6	ABQ80576	88.0	2853	5	Abq80576 ABN58052
c 15	17.6	ABQ80577	88.0	11275	6	Abq80577 ABN58052
c 16	16.6	ABQ80578	83.0	4689	8	Abq80578 ABN58052
c 17	16.6	ABQ80579	83.0	110000	4	Abq80579 ABN58052
c 18	16.6	ABQ80580	83.0	110000	4	Abq80580 ABN58052
c 19	16.4	ABQ80581	82.0	1520	6	Abq80581 ABN58052
c 20	16.4	ABQ80582	82.0	1520	6	Abq80582 ABN58052

ALIGNMENTS

RESULT 1
ID AAF79959 Standard; DNA; 20 BP.
XX AAF79959;
XX AC
DT 11-JUN-2001 (first entry)
XX DE PCR primer used to amplify trimethylamine N-oxide reductase genes.
XX KW tora gene; trimethylamine N-oxide reductase; flesh degradation;
KW spoilage bacteria; fish; crustacean; PCR primer; ss.
OS Synthetic.
XX PN WO20030-A2.
XX WO20030-A2.
PD 22-MAR-2001.
XX PP 15-SEP-2000; 2000WO-PR02578.
XX PR 15-SEP-1999; 99FR-00011543.
XX (CNRS) CENT NAT RECH SCI.
XX PA Giordano G, Dos Santos J, Mejean V;
XX DR WPI ; 2001-244822/25.
XX PD Detecting bacteria that cause flesh degradation in fish, for testing
PT freshness, comprises using probes or primers based on the trimethylamine
PT N-oxide reductase system.
PS Claim 7; Page 42; 91PP; French.

XX PCR primers AAP79951-66 represent PCR primers used to amplify torA and
CC torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
CC oxide reductase system. TorA nucleic acids are used for detecting, in a
CC

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CDM nucleic - nucleic search, using sw mode!

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
(without alignments)

5660.438 Million cell updates/sec

Title: US-10-088-117A-20

Perfect score: 20

Sequence: 1 twygarcgyaacgaymtcga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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	C	28	16	80.0	725	5
	C	29	16	80.0	776	7
	C	30	16	80.0	803	4
	C	31	16	80.0	896	4
	C	32	16	80.0	970	9
	C	33	16	80.0	1118	7
	C	34	15.6	78.0	347	5
	C	35	15.6	78.0	367	8
	C	36	15.6	78.0	526	4
	C	37	15.6	78.0	530	1
	C	38	15.6	78.0	624	8
	C	39	15.6	78.0	653	9
	C	40	15.6	78.0	762	8
	C	41	15.6	78.0	824	2
	C	42	15.6	78.0	830	9
	C	43	15.6	78.0	892	2
	C	44	15.6	78.0	1015	8
	C	45	15.4	77.0	242	6
	C	46	15.4	77.0	400	5
	C	47	15.4	77.0	448	5
	C	48	15.4	77.0	499	7
	C	49	15.4	77.0	520	105
	C	50	15.4	77.0	555	5

SILENT ALIGNMENTS

Result No.	Score	Match	Length	DB	ID	Description	Query Match			Best Local Similarity			Query Match			Best Local Similarity		
							Source	Location/Qualifiers	Accession	Matches	Prd. No.	Mismatches	Source	Location/Qualifiers	Accession	Matches	Prd. No.	Mismatches
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c	2	16.4	82.0	100	6	AX989852	Sequence	AX989852	/mol type="unassigned DNA"		100.0%	Prd. No. 3.e+02;	Db	1	GGTVCATACABSSCCCTTC	20		
c	3	16.4	82.0	100	6	AX997781	Sequence	AX997781	/db Xref="Taxon:12630"									
c	4	16.4	82.0	2475	6	AX098610	Sequence	AX098610	/notes="amore PCR"									
c	5	16.4	82.0	2486	6	AX098605	Sequence	AX098605										
c	6	16.4	82.0	2487	6	AX098604	Sequence	AX098604										
c	7	16.4	82.0	2487	6	AX098604	Sequence	AX098604										
c	8	16.4	82.0	2490	1	SPU5974	Sequence	SPU5974										
c	9	16.4	82.0	2540	1	RCDSTNORG	Sequence	RCDSTNORG										
c	10	16.4	82.0	2544	6	AX098612	Sequence	AX098612										
c	11	16.4	82.0	3211	1	ECOCBPA	Sequence	ECOCBPA										
c	12	16.4	82.0	4680	1	RCTOR	Sequence	RCTOR										
c	13	16.4	82.0	5637	1	RCU49506	Sequence	RCU49506										
c	14	16.4	82.0	6492	1	ECODMS	Sequence	ECODMS										
c	15	16.4	82.0	6511	1	SMA6085	Sequence	SMA6085										
c	16	16.4	82.0	9994	1	AE001576	Sequence	AE001576										
c	17	16.4	82.0	10726	1	AE015567	Sequence	AE015567										
c	18	16.4	82.0	11860	1	U32747	Sequence	U32747										
c	19	16.4	82.0	12302	1	AEO15779	Sequence	AEO15779										
c	20	16.4	82.0	12582	1	AE015114	Sequence	AE015114										
c	21	16.4	82.0	13067	1	AE015128	Sequence	AE015128										
c	22	16.4	82.0	16210	1	D90727	Sequence	D90727										
c	23	16.4	82.0	18252	1	D90737	Sequence	D90737										
c	24	16.4	82.0	19650	1	D90736	Sequence	D90736										
c	25	16.4	82.0	24418	1	AE00878	Sequence	AE00878										
c	26	16.4	82.0	254050	1	AE00741	Sequence	AE00741										
c	27	16.4	82.0	110000	1	U0006_09	Sequence	U0006_09										
c	28	16.4	82.0	110000	1	U0006_10	Sequence	U0006_10										
c	29	16.4	82.0	110000	6	BD42631_06	Sequence	BD42631_06										
c	30	16.4	82.0	110000	6	AR27451_06	Sequence	AR27451_06										
c	31	16.4	82.0	110000	6	AR54453_06	Sequence	AR54453_06										
c	32	16.4	82.0	245050	1	AL627280_	Sequence	AL627280										
c	33	16.4	82.0	250950	1	AP005335	Sequence	AP005335										
c	34	16.4	82.0	291504	1	AB016381	Sequence	AB016381										
c	35	16.4	82.0	294050	1	AL627268	Sequence	AL627268										
c	36	16.4	82.0	297808	1	AP00553	Sequence	AP00553										
c	37	16.4	82.0	299130	1	AP005077	Sequence	AP005077										
c	38	16.4	82.0	300592	1	AB016846	Sequence	AB016846										
c	39	16.4	82.0	301276	1	AE016758	Sequence	AE016758										
c	40	16.4	82.0	301983	1	AB016840	Sequence	AB016840										
c	41	16.4	82.0	304490	1	AE016806	Sequence	AE016806										
c	42	16.4	82.0	349080	1	CR378667	Sequence	CR378667										
c	43	15.6	78.0	110000	1	AB01154_	Sequence	AB01154_										
c	44	15.6	78.0	300540	1	AL139074	Sequence	AL139074										
c	45	15.6	78.0	314150	1	CJ11168X1	Sequence	CJ11168X1										
c	46	15.6	78.0	348672	1	CR378670	Sequence	CR378670										
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c	48	15.4	77.0	10447	1	AB00556	Sequence	AB00556										
c	49	15.4	77.0	153500	6	BD269447	Sequence	BD269447										
ALIGNMENTS																		
RESULTS																		
SUMMARIES																		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.																		
SUMMARY																		
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2: genesegm1990s;
3: genesegm2000s;*
4: genesegm2001as;*
5: genesegm2001bs;*
6: genesegm2002as;*
7: genesegm2002bs;*
8: genesegm2003as;*
9: genesegm2003bs;*
10: genesegm2003cs;*
11: genesegm2003ds;*
12: genesegm2004as;*
13: genesegm2004bs;*

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SUMMARIES

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c	16.4	82.0	100	8 ACD79945	Acd79945 B. coli K
c	16.4	82.0	1338	5 AAS83390	Aas83390 DNA endonuclease
c	16.4	82.0	1887	4 AAH19221	Aah19221 Human sec
c	16.4	82.0	2358	8 ACA19185	Aca19185 Prokaryot
c	16.4	82.0	2358	13 ADS6037	Ado6037 Bacterium
c	16.4	82.0	2413	8 ACA43353	Aca43353 Prokaryot
c	16.4	82.0	2445	8 ACA51180	Aca51180 Prokaryot
c	16.4	82.0	2445	8 ACA51914	Aca51914 Prokaryot
c	16.4	82.0	2475	4 AAF79948	Aaf79948 Nucleotid
c	16.4	82.0	2486	4 AAF79944	Aaf79944 Nucleotid
c	16.4	82.0	2487	4 AAF79945	Aaf79945 Nucleotid
c	16.4	82.0	2487	4 AAF79943	Aaf79943 Nucleotid
c	16.4	82.0	2544	4 AAF79949	Aaf79949 Nucleotid
c	16.4	82.0	2547	13 ADS60464	Ado60464 Bacterium
c	16.4	82.0	3712	4 AAH41184	Aah41184 Human sec
c	16.4	82.0	11275	6 AAH41717	Aah41717 E. coli K
c	16.4	82.0	110000	2 ART43063_06	Art43063_06
c	15.4	77.0	1641	3 AAC55833	Aac55833 S. lavendulae

				S. laven-
21	15.4	77.0	1641	10 Ade10252
22	15.4	77.0	53500	3 AAC5542
23	15.4	77.0	53500	10 Ade10461
24	14.8	74.0	129	5 ABA15064
25	14.8	74.0	395	8 ABX45119
26	14.8	74.0	442	8 ABX46038
27	14.8	74.0	519	8 ABZ53408
28	14.8	74.0	804	5 AAS85035
29	14.8	74.0	1176	5 AAS65036
30	14.8	74.0	1597	13 ADS48720
31	14.8	74.0	1794	3 AAA30216
32	14.8	74.0	1913	13 ACN3272
33	14.8	74.0	2268	8 ACA31543
34	14.8	74.0	2280	13 ABD31563
35	14.8	74.0	2286	12 ADIB1563
36	14.8	74.0	2286	12 ADIB1575
37	14.8	74.0	2289	12 ADIB1627
38	14.8	74.0	2310	6 AAD9472
39	14.8	74.0	2319	6 ABZ82575
40	14.8	74.0	2436	8 ACA35519
41	14.8	74.0	2478	11 ACH99175
42	14.8	74.0	2523	4 AAP79947
43	14.8	74.0	2597	6 ABK70006
44	14.8	74.0	2597	9 ADA01559
45	14.8	74.0	2597	9 ADA43788
46	14.8	74.0	2597	9 ADA43556
47	14.8	74.0	2597	9 ADA01231
48	14.8	74.0	2597	9 ADA01115
49	14.8	74.0	2597	9 ADA36712
50	14.8	74.0	2597	9 ADA05634

ALIGNMENTS

RESULT 1
 AAF79960
 ID AAF79960 standard; DNA; 20 BP.
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 AC
 AAF79960;
 XX
 DT
 DE
 XX
 XX
 .11-JUN-2001 (First entry)
 PCR primer used to amplify trimethylamine N-oxide reductase genes.
 tora gene; trimethylamine N-oxide reductase; flesh degradation;
 spoilage bacteria; fish; crustacean; PCR prime; ss.

Synthetic.
WO200120030-A2.
22-MAR-2001.
15-SEP-2000; 2000WO-FR002578.
15-SEP-1999; 99FR-00011543.
(CNRS) CENT NAT RECH SCI.
Giordano G, Dos Santos J, Mejean V;
WPI; 2001-244022/25.

Detecting bacteria that cause flesh degradation in fish, for testing freshness, comprises using probes or primers based on the trimethylamine N-oxide reductase system.

Claim 7: Page 42; 91pp; French.

PCR primers ARF79951-66 represent PCR primers used to amplify torA and torC genes. TorA and torC are bacterial proteins of the trimethylamine N-oxide reductase system. TorA nucleic acids are used for detecting in a

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OM nucleic - nucleic search, using sw mode!

Run on: June 2, 2005, 08:20:11 ; Search time 6.17692 Seconds

(without alignments)

5298.032 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggvcrtaccabscvcccttc 20

Scoring table: IDENTITY_NUC

Gapext 1.0

Score: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters:

2405558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Issued_Patents_NA:
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 2: /cgn2_6/picodata/1/ina/5B_COMB.seq:
 3: /cgn2_6/picodata/1/ina/6A_COMB.seq:
 4: /cgn2_6/picodata/1/ina/6B_COMB.seq:
 5: /cgn2_6/picodata/1/ina/PCITS_COMB.seq:
 6: /cgn2_6/picodata/1/ina/backfiles.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	16.4	82.0	180121	4	US-09-557-884-1		Sequence 1, Appli	
2	16.4	82.0	180121	4	US-09-643-990A-1		Sequence 1, Appli	
3	15.4	77.0	1641	4	US-09-266-955-67		Sequence 67, Appli	
4	15.4	77.0	31500	4	US-09-266-955-76		Sequence 76, Appli	
c	14.8	74.0	2478	4	US-09-189-039A-4970		Sequence 4970, Appli	
6	14.8	74.0	2736	3	US-09-235-411-3		Sequence 3, Appli	
7	14.8	74.0	2736	3	US-09-235-411-3		Sequence 3, Appli	
c	8	14.4	72.0	654	4	US-09-978-303-3		Sequence 72, Appli
c	9	14.4	72.0	1305	4	US-09-302-540-6383		Sequence 6383, Appli
c	10	14.4	72.0	2492	4	US-09-940-421-1		Sequence 421, Appli
c	11	14.4	72.0	128516	4	US-09-149-016-1301		Sequence 13501, Appli
c	12	14.4	72.0	133157	4	US-09-949-016-12541		Sequence 12541, Appli
c	13	14.2	71.0	3343	4	US-09-503-880-1		Sequence 1, Appli
c	14	14.2	70.0	307	4	US-09-921-976-11201		Sequence 11201, Appli
c	15	14	70.0	601	4	US-09-949-016-67294		Sequence 67294, Appli
c	16	14	70.0	2451	4	US-09-543-601A-427		Sequence 427, Appli
c	17	14	70.0	3425	4	US-09-800-971-1		Sequence 1, Appli
c	18	14	70.0	13953	3	US-09-738-884-3		Sequence 3, Appli
c	19	14	70.0	13953	4	US-10-096-961A-3		Sequence 3, Appli
c	20	14	70.0	36307	4	US-09-949-016-12372		Sequence 17372, Appli
c	21	14	70.0	100463	4	US-09-949-016-12511		Sequence 12511, Appli
c	22	14	70.0	100468	4	US-09-949-016-13725		Sequence 13725, Appli
c	23	14	70.0	139560	4	US-09-949-016-17202		Sequence 17202, Appli
c	24	13.8	69.0	219	4	US-09-489-039A-7065		Sequence 7065, Appli
c	25	13.8	69.0	601	4	US-09-949-016-13521		Sequence 13521, Appli
c	26	13.8	69.0	601	4	US-09-949-016-170678		Sequence 170678, Appli
c	27	13.8	69.0	647	4	US-09-777-430C-72		Sequence 777, Appli

Sequence 104, App
Sequence 3, Appli
Sequence 1341, App
Sequence 25, Appli
Sequence 1165, App
Patent No. 5121073
Patent No. 5121073
Sequence 1, Appli
Sequence 6085, App
Sequence 267, App
Sequence 106, App
Sequence 105, App
Sequence 306, App
Sequence 308, App
Sequence 534, App
Sequence 53, App
Sequence 1530, A
Sequence 12634, A
Sequence 16565, A
Sequence 16727, A
Sequence 17, Appi
Sequence 16346, A

ALIGNMENTS

RESULT 1
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; GENERAL APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIAN TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-557-884-1

			Sequence 67, App1
			Sequence 67, App1
			Sequence 67, App1
			Sequence 76, App1
			Sequence 76, App1
12	15.4	77.0	US-09-953-348-67
	13	15.4	1641 10 US-10-267-255-67
	14	15.4	1641 15 US-10-9-952-348-76
	15	15.4	53500 10 US-10-267-255-76
	c	16	14.8 14461 14 US-10-741-601-148486
	c	17	14.8 201 18 US-10-741-600-37981
	c	18	14.8 201 19 US-10-741-600-37981
	c	19	14.8 376 18 US-10-0-245-1-15-45319
	c	20	14.8 74.0 9 US-09-960-352-1-0284
	c	21	14.8 74.0 442 9 US-09-960-352-1-1223
	c	22	14.8 74.0 517 13 US-10-0-27-632-128865
	c	23	14.8 74.0 656 17 US-10-0-27-632-128865
	c	24	14.8 74.0 719 13 US-10-0-27-632-26875
	c	25	14.8 74.0 719 17 US-10-0-27-632-26667
	c	26	14.8 74.0 769 13 US-10-0-27-632-15109
	c	27	14.8 74.0 769 17 US-10-0-27-632-15109
	c	28	14.8 74.0 804 18 US-10-0-37-963-94508
	c	29	14.8 74.0 1541 17 US-10-0-25-114-15108
	c	30	14.8 74.0 1597 17 US-10-369-493-27150
	c	31	14.8 74.0 1615 19 US-10-0-24-539-26866
	c	32	14.8 74.0 1937 19 US-10-0-887-553-0-387
	c	33	14.8 74.0 2268 17 US-10-0-282-122A-19413
	c	34	14.8 74.0 2280 18 US-10-322-251-765
	c	35	14.8 74.0 2286 17 US-10-0-342-844-33
	c	36	14.8 74.0 2286 17 US-10-342-844-45
	c	37	14.8 74.0 2289 17 US-10-342-844-97
	c	38	14.8 74.0 2310 16 US-10-240-965-7
	c	39	14.8 74.0 2436 17 US-10-282-122A-23389
	c	40	14.8 74.0 2597 14 US-10-245-752-91
	c	41	14.8 74.0 2597 14 US-10-245-859-91
	c	42	14.8 74.0 2597 14 US-10-245-103-91
	c	43	14.8 74.0 2597 14 US-10-245-107-91
	c	44	14.8 74.0 2597 14 US-10-245-143-91
	c	45	14.8 74.0 2597 14 US-10-245-771-91
	c	46	14.8 74.0 2597 14 US-10-245-851-91
	c	47	14.8 74.0 2597 14 US-10-245-983-91
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	c	50	14.8 74.0 2597 14 US-10-238-183-91

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Score	Match	Length	DB	ID	Description
1	16.4	82.0	264	17	US-10-335-977-1903	Sequence 1903, AP
2	16.4	82.0	348	17	US-10-335-977-1904	Sequence 1904, AP
3	16.4	82.0	2358	17	US-10-367-493-24467	Sequence 24467, A
4	16.4	82.0	2358	17	US-10-282-122A-7055	Sequence 7055, AP
5	16.4	82.0	2413	17	US-10-282-122A-37223	Sequence 37223, A
6	16.4	82.0	2445	17	US-10-282-122A-39050	Sequence 39050, A
7	16.4	82.0	2445	17	US-10-282-122A-39784	Sequence 39784, A
8	16.4	82.0	2547	17	US-10-369-493-24476	Sequence 24476, A
9	16.4	82.0	11275	16	US-10-240-689-39	Sequence 39, Appl
10	16.4	82.0	1830121	17	US-10-329-670-1	Sequence 1, Appl
11	16.4	82.0	1830121	18	US-10-158-805-1	Sequence 1, Appl

RESULT¹
US-10-335-977-1903/c
Sequence 1903, Application US 10335977
Publication No. US2004005279981
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISCR9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993, 002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:

SUMMARIES

Score. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 5.1.6	CN702732	E0465H1	CNT02732		
Copyright (c) 1993 - 2005 Compugen Ltd.	CF741585	UI-M-HB	CF741585		
nucleic - nucleic search, using sw model	CO429861	UI-M-HX	CO429861		
on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds (without alignments)	CA242359	SCEPPUJ3	CA242359		
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Influence: 1.99vvccatccaccvcccttc 20	CK534748	VI-M-HN	CK534748		
String table: IDENTITY_NUC	CK534748	VI-M-HN	CK534748		
Gapop 10_0 , Gapext 1.0	CK534748	VI-R-FJ	CK534748		
Searched: 34239544 seqs, 19032134700 residues	CK534748	VI-R-YO	CK534748		
Actual number of hits satisfying chosen parameters: 68479088	CK534748	QV2-BT0	CK534748		
Minimum DB seq length: 0	CK534748	SP	CK534748		
Maximum DB seq length: 2000000000	CK534748	Ba00126	CK534748		
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Maximum Match 100%	CK534748	CM4-MT0	CK534748		
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2: gb_est2:*	CK534748	AA321284	CK534748		
3: gb_htc:*	CK534748	BB401766	CK534748		
4: gb_est3:*	CK534748	BZ943315	CK534748		
5: gb_est4:*	CK534748	CH240-8	CK534748		
6: gb_est5:*	CK534748	CB108935	CK534748		
7: gb_est6:*					
8: gb_gss1:*					
9: gb_gss2:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
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1	16.4	82.0	700	1 AL509140	AL509140 mRNA linear EST 04-JAN-04
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3	16.4	82.0	786	9 CL666247	CL666247 PR0151d
4	16.4	82.0	847	3 CL670484	PR0162b
5	15.6	78.0	362	6 BY657438	BY657438
6	15.6	78.0	434	5 BY461297	BY461297
7	15.6	78.0	613	2 BB651761	BB651761
8	15.4	77.0	214	2 BB216706	BB216706
9	15.4	77.0	452	7 CK526609	CK526609
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11	15.4	77.0	756	9 AG593385	AG593385
12	15.4	77.0	853	6 CD751046	CD751046
13	15.4	77.0	877	2 BF623577	BF623577
14	15.4	77.0	953	7 CP455917	CP455917
15	15.4	77.0	1070	7 CP455948	CP455948
16	15.4	77.0	1083	5 BQ815751	BQ815751
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18	15.2	76.0	296	2 BF551618	BF551618
19	15.2	76.0	432	9 CL214740	CL214740
20	15.2	76.0	583	5 BUT02144	BUT02144
21	15.2	76.0	599	7 CB892278	CB892278
22	15.2	76.0	608	9 CCB75829	CCB75829
23	15.2	76.0	624	7 CP727912	CP727912
24	15.2	76.0	626	7 CR894749	CR894749
AL509140	AL509140	AL509140	AL509140	AL509140	AL509140
LOCUS	AL509140	AL509140	AL509140	AL509140	AL509140
DEFINITION	Hordeum vulgare Barke developing caryopsis				
KEYWORDS	EST.	EST.	EST.	EST.	EST.
ORGANISM	Hordeum vulgare subsp. vulgare				
SEQUENCE	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
VERSION	AL509140.1	AL509140.1	AL509140.1	AL509140.1	AL509140.1
COMMENT	Unpublished (2000)				
CONTACT	Michael W. Weichke				
INSTITUTE	Institute for Plant Genetics and Crop Plant Research	Institute for Plant Genetics and Crop Plant Research	Institute for Plant Genetics and Crop Plant Research	Institute for Plant Genetics and Crop Plant Research	Institute for Plant Genetics and Crop Plant Research
CORRESPONDING_AUTHOR	Corrensstr. 3, D-06466 Gatersleben, Germany				
EMAIL	mailto:michael@ipk-gatersleben.de	mailto:michael@ipk-gatersleben.de	mailto:michael@ipk-gatersleben.de	mailto:michael@ipk-gatersleben.de	mailto:michael@ipk-gatersleben.de
SEQ_PRIM	T3 primer for 5'-end.				
FEATURES	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers
Source	1..700	1..700	1..700	1..700	1..700
Organism	/organism="Hordeum vulgare subsp. vulgare"				
Mol_Type	/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"
Cultivar	/cultivar="Barke"	/cultivar="Barke"	/cultivar="Barke"	/cultivar="Barke"	/cultivar="Barke"
Sub_Species	/sub_species="vulgare"	/sub_species="vulgare"	/sub_species="vulgare"	/sub_species="vulgare"	/sub_species="vulgare"
Db_Xref	/db_xref="taxon:112509"	/db_xref="taxon:112509"	/db_xref="taxon:112509"	/db_xref="taxon:112509"	/db_xref="taxon:112509"
Cloner	/cloner="H110N07V"	/cloner="H110N07V"	/cloner="H110N07V"	/cloner="H110N07V"	/cloner="H110N07V"
Tissue_Type	/tissue_type="developing caryopsis"				
Lab_Host	/lab_host="XLORF"	/lab_host="XLORF"	/lab_host="XLORF"	/lab_host="XLORF"	/lab_host="XLORF"
Clone_Lib	/clone_lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"				
Note	/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XbaI; mRNA was made from developing caryopsis (3.-15.DA) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XbaI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present as well as the XbaI cleavage site. Average insert size: 1.5 kb."	/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XbaI; mRNA was made from developing caryopsis (3.-15.DA) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XbaI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present as well as the XbaI cleavage site. Average insert size: 1.5 kb."	/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XbaI; mRNA was made from developing caryopsis (3.-15.DA) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XbaI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present as well as the XbaI cleavage site. Average insert size: 1.5 kb."	/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XbaI; mRNA was made from developing caryopsis (3.-15.DA) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XbaI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present as well as the XbaI cleavage site. Average insert size: 1.5 kb."	/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XbaI; mRNA was made from developing caryopsis (3.-15.DA) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XbaI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present as well as the XbaI cleavage site. Average insert size: 1.5 kb."

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds

(without alignments)

6151.841 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 attacccatggcggtgcc 20

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 4708333 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:

9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Lining First 50 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_heg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	16.6	83.0	20 AX098625	AX098625 Sequence
c 2	16.6	83.0	2292 U25037	U25037 Rhodobacter
c 3	16.6	83.0	2475 AX098610	AX098610 Sequence
c 4	16.6	83.0	2486 AX098605	AX098605 Sequence
c 5	16.6	83.0	2487 AX098604	AX098604 Sequence
c 6	16.6	83.0	2487 AX098606	AX098606 Sequence
c 7	16.6	83.0	2490 AJ05374	AJ05374 Shewanell
c 8	16.6	83.0	2523 AX098609	AX098609 Sequence
c 9	16.6	83.0	2540 R.CDSINORG	X95407 R.capsulatus
c 10	16.6	83.0	2544 AX098612	AX098612 Sequence
c 11	16.6	83.0	2750 RCADSRA	146851 Rhodobacter
c 12	16.6	83.0	3316 RCADMS	D38634 Rhodobacter
c 13	16.6	83.0	4680 RCTOR	X74888 E.coli gene
c 14	16.6	83.0	5637 RCT49506	U49506 Rhodobacter
c 15	16.6	83.0	6915 SRA6085	AJ006085 Shewanell
c 16	16.6	83.0	7990 AF016236	AF016236 Rhodobacter
c 17	16.6	83.0	10726 AE015567	AE015567 Shewanell
c 18	16.6	83.0	11289 AE005233	AE005233 Escherich
c 19	16.6	83.0	13067 AE015128	AE015128 Shigella

D90737	Escherichia
D90736	Escherichia
Continuation (11 o	
AC010537	Homo sapi
AE016391	Shigella
AE016758	Escherich
AP005958	Bradyrhiz
AP002554	Escherich
AX098613	Sequence
AL445215	Human DNA
AL6227280	Salmonell
AE016846	Salmonell
BV200860	seqnm20519
BV200998	seqnm20557
BD135671	Observati
AX321171	Sequence
BD180449	Highly th
AB107688	Thermus t
AX885383	Sequence
BD024993	Sequence
BT007045	Homo sapi
CR541718	Human DNA
AY335665	Synthetic
AX321130	Sequence
AX3211420	Sequence
AX381521	Sequence
AX321189	Sequence
AF043542	Gallus ga
BD079935	Cancer-as

ALIGNMENTS

RESULT	1	AX098625	Sequence 22 from Patent WO0120030.	20 bp	DNA	linear	PAT 02-APR-2001
LOCUS	AX098625	DEFINITION	Sequence 22 from Patent WO0120030.				
ACCESSION	AX098625	VERSION	AX098625.1	GI:11537886			
VERSION	AX098625.1	SOURCE					
ORGANISM		synthetic construct					
ORGANISM		synthetic construct					
OTHER SEQUENCES		other sequences; artificial sequences.					
REFERENCE	1	Giordano,G., dos Santos,J.P. and Mejean,V.					
AUTHORS		Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria					
JOURNAL	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)	LOCATION/QUALIFIERS					
FEATURES	Source	1. 20					
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	/mol_type="unassigned DNA"						
	/db_xref="taxon:32630"						
	/note="amorce PCR"						
ORIGIN							
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Best Local Similarity	100.0%	Pred. No. 2.6e-03;	Mismatches 0;	Indels 0;	Gaps 0;		
Matches 20;	Conservative						

Qy	1 ATCARRCCNSWVGCGTGGCC 20
Db	1 ATCARRCCNSWVGCGTGGCC 20
RESULT	2
RSU25037/c	RSU25037
LOCUS	RSU25037

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OM nucleic - nucleic search, using SW model

Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds

5926.580 Million cell updates/sec
1 atccarrccnswvvgcggtggc 20

Title: US-10-088-117A-22
Perfect score: 20

Sequence: 1 atccarrccnswvvgcggtggc 20

Scoring table: IDENTITY_NUC

Gapon 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 50 summaries

Database : N_GeneseqN_16Dec04:*

1: GeneseqN1900B:*

2: GeneseqN1900B:*

3: GeneseqN2000B:*

4: GeneseqN2001B:*

5: GeneseqN2001B:*

6: GeneseqN2002as:*

7: GeneseqN2002bs:*

8: GeneseqN2003as:*

9: GeneseqN2003bs:*

10: GeneseqN2003cb:*

11: GeneseqN2003ds:*

12: GeneseqN2004as:*

13: GeneseqN2004bs:*

21	15.6	78.0	576	13	AD545929	Bacterial	
22	15.6	78.0	599	6	AAS31665	Lung small	
23	15.6	78.0	647	2	AAC0201	Gene encod	
24	15.6	78.0	670	3	AAT0315	Human nm2	
25	15.6	78.0	670	6	AAL53615	CDNA encod	
26	15.6	78.0	670	6	AAI17922	Human NM2	
27	15.6	78.0	670	8	ACG89880	Gene diff	
28	15.6	78.0	670	10	ADH28764	Human chr	
29	15.6	78.0	670	12	ADH17090	Human nm2	
30	15.6	78.0	670	13	ADR24919	Breast ca	
31	15.6	78.0	670	13	ACM40229	Tumour-as	
32	15.6	78.0	670	13	ADP23161	PRO polyP	
33	15.6	78.0	670	13	ADR65896	Human pro	
34	15.6	78.0	670	13	ADR666799	Human ORP	
35	15.6	78.0	1680	4	AAR41415	Aah41415	
36	15.6	78.0	5070	11	ADN95692	Human BBC	
37	15.6	78.0	5071	12	ADQ18401	Human sof	
38	15.6	78.0	5123	13	ADT07187	Full leng	
39	15.6	78.0	10820	6	AB19492	Mouse isoC	
C	40	15.4	77.0	256	ABN18266	Abn18266	
c	41	15.0	75.0	573	8	ACG39660	Prokaryot
c	42	15.0	75.0	1284	11	ACN44221	Acn44221
c	43	15.0	75.0	1431	3	AAM51612	Mouse mRN
c	44	15.0	75.0	1437	3	AAM51619	HIV gp120
c	45	15.0	75.0	1944	3	AAM51613	HIV gp140
c	46	15.0	75.0	1950	3	AAM51620	HIV gp140
c	47	15.0	75.0	2466	3	AAM51614	HIV gp160
c	48	15.0	75.0	2493	3	AAM51621	HIV gp160
c	49	15.0	75.0	2547	3	AAM51615	HIV gp160
c	50	15.0	75.0	2550	6	AAL44550	HIV-1 env

ALIGNMENTS

RESULT 1
ID AAF79961 standard; DNA; 20 BP.
XX
AC AAF79961;
XX DT 11-JUN-2001 (first entry)
XX DR PCR primer used to amplify trimethylamine N-oxide reductase genes.
XX torA gene; trimethylamine N-oxide reductase; flesh degradation;
XX spoilage bacteria; fish; crustacean; PCR primer; ss.
XX Synthetic.
XX OS

%
Pred No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	16.6	83.0	20	4	AAF79961	AAF79961 PCR prime
c. 2	16.6	83.0	2475	4	AAF79948	Aaf79948 Nucleotid
c. 3	16.6	83.0	2486	4	AAF79944	Aaf79944 Nucleotid
c. 4	16.6	83.0	2487	4	AAF79945	Aaf79945 Nucleotid
c. 5	16.6	83.0	2523	4	AAF79943	Aaf79943 Nucleotid
c. 6	16.6	83.0	2544	4	AAF79947	Aaf79947 Nucleotid
c. 7	16.6	83.0	2547	13	ADS46046	Adbs46046 Bacterial
c. 8	16.6	83.0	2547	13	AAS72908	Aas72908 DNA encod
c. 9	16.6	83.0	2853	5	AAS93063	Aas93063 DNA encod
c. 10	16.6	83.0	2853	5	AAS92727	Aas92727 DNA encod
c. 11	16.6	83.0	2853	5	AAS86655	Aas86655 DNA encod
c. 12	16.6	83.0	11275	6	AAR43717	Aar43717 E. coli g
c. 13	16.6	83.0	477	4	AAF79950	Aaf79950 Partial n
c. 14	15.6	79.0	303	6	ABK93063	Abk93063 cDNA encod
c. 15	15.6	78.0	376	6	AAS61647	Aas61647 Lung small
c. 16	15.6	78.0	445	3	AAC01248	Aac01248 Human sec
c. 17	15.6	78.0	501	6	AAS61506	Aas61506 Lung email
c. 18	15.6	78.0	501	6	AAS61871	Aas61871 Lung small
c. 19	15.6	78.0	518	6	ABK55059	Abk55059 Human col

Claim 7; Page 42; 91pp; French.
XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
oxide reductase system. TorA nucleic acids are used for detecting, in a

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 6.17692 seconds
 (without alignments)

5298.032 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atccarrccnswggctgccc 20

Scoring table: IDENTITY NUC Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 50 summaries

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTM6_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	601	4 US-09-949-016-145811	Sequence 145811,
C 2	15.8	79.0	601	4 US-09-949-016-146079	Sequence 146079,
C 3	15.8	79.0	601	4 US-09-949-016-146347	Sequence 146347,
C 4	15.8	79.0	205044	4 US-09-949-016-15851	Sequence 15851,
C 5	15.8	79.0	205044	4 US-09-949-016-15852	Sequence 15852,
C 6	15.8	79.0	205044	4 US-09-949-016-15853	Sequence 15853,
C 7	15.8	79.0	223471	4 US-09-949-016-12387	Sequence 12387,
C 8	15.8	79.0	223471	4 US-09-949-016-12724	Sequence 12724,
C 9	15.8	78.0	223471	4 US-09-949-016-12225	Sequence 12725,
C 10	15.6	78.0	445	4 US-09-513-999C-1246	Sequence 1246,
C 11	15.6	78.0	670	3 US-09-33-948-3	Sequence 3,
C 12	15.6	78.0	670	3 US-07-006-922B-4	Sequence 4,
C 13	15.6	78.0	4316	4 US-09-949-016-12387	Sequence 5750,
C 14	15.6	78.0	5071	4 US-09-949-016-363	Sequence 363,
C 15	15.6	78.0	10302	4 US-09-949-016-17492	Sequence 17492,
C 16	15.6	75.0	131332	4 US-09-153-948-3	Sequence 15535,
C 17	14.6	73.0	465	4 US-09-107-52A-2346	Sequence 2346,
C 18	14.6	73.0	825	4 US-09-902-540-4480	Sequence 4480,
C 19	14.6	73.0	921	4 US-09-952-951A-210	Sequence 146079,
C 20	14.6	73.0	1019	3 US-09-183-861-19	Sequence 19,
C 21	14.6	73.0	1019	3 US-09-022-755-19	Sequence 19,
C 22	14.6	73.0	1019	4 US-09-551-974A-19	Sequence 19,
C 23	14.6	73.0	1019	4 US-09-565-501A-19	Sequence 19,
C 24	14.6	73.0	1019	4 US-09-639-206A-19	Sequence 19,
C 25	14.6	73.0	1019	4 US-09-74-93-19	Sequence 19,
C 26	14.6	73.0	1019	4 US-08-798-801-19	Sequence 19,
C 27	14.6	73.0	1026	4 US-09-252-991A-2172	Sequence 2172,

RESULT 1

US-09-949-016-145811/C
 ; Sequence 145811, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09-949-016-145811
 ; PRIORITY APPLICATION NUMBER: 60/104-14
 ; PRIORITY FILING DATE: 2000-10-20
 ; PRIORITY NUMBER: 60/237,768
 ; PRIORITY FILING DATE: 2000-10-03
 ; PRIORITY APPLICATION NUMBER: 60/231,498
 ; CURRENT FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 145811
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-145811

Query Match Score 15.8; DB 4; Length 601;
 Best Local Similarity 70.0%; Pred. No. 53;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATCARRCCNSWGGCTGCCC 20
 ||||| : : |||||
 Db 234 ATCAAGCCCCCTGGCTGCCC 215

RESULT 2

US-09-949-016-14079/C
 ; Sequence 146079, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 21.2846 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atccarrccnswwgcgtgcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 50 summaries

Database : Published Applications_NP_*

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4: /cgm2_6/_ptodata/2/_pubna/_US06_PUBCOMB.seq;*
5: /cgm2_6/_ptodata/2/_pubna/_US07_NEW_PUB.seq;*
6: /cgm2_6/_ptodata/2/_pubna/_PCTUS_PUBCOMB.seq;*
7: /cgm2_6/_ptodata/2/_pubna/_US08_NEW_PUB.seq;*
8: /cgm2_6/_ptodata/2/_pubna/_US08_PUBCOMB.seq;*
9: /cgm2_6/_ptodata/2/_pubna/_US09_NEW_PUBCOMB.seq;*
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12: /cgm2_6/_ptodata/2/_pubna/_US10A_PUBCOMB.seq;*
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16: /cgm2_6/_ptodata/2/_pubna/_US10B_PUBCOMB.seq;*
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19: /cgm2_6/_ptodata/2/_pubna/_US10_NEW_PUB.seq;*
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21: /cgm2_6/_ptodata/2/_pubna/_US60_NEW_PUB.seq;*
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RESULT 1
US-10-369-493-24476.C
/ Sequence 24476, Application US/10369493
/ Publication No. US2003033675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
/ FILE REFERENCE: 38-101520521B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 24476

SUMMARIES

Result No.	Score	Query Match	Length	DB . ID	Description
c 1	16.6	83.0	2547	17 US-10-369-493-24476	Sequence 24476, A
c 2	16.6	83.0	11275	16 US-10-240-689-39	Sequence 39, Appl
c 3	15.6	78.0	376	9 US-09-833-790-188	Sequence 188, Appl
4	15.6	78.0	456	17 US-10-133-628-9	Sequence 9, Appl
5	15.6	78.0	456	17 US-10-133-628-10	Sequence 10, Appl
6	15.6	78.0	501	9 US-09-833-790-147	Sequence 147, Appl
7	15.6	78.0	501	9 US-09-833-790-437	Sequence 437, Appl
8	15.6	78.0	518	9 US-09-919-580-529	Sequence 529, APP
9	15.6	78.0	576	17 US-10-369-493-24359	Sequence 24359, A
10	15.6	78.0	599	9 US-09-833-790-206	Sequence 206, APP
11	15.6	78.0	670	15 US-10-171-581-32	Sequence 32, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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CM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds

(without alignments)

5660.438 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atccatcccttggcggtgcc 20

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

68479088 Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 50 summaries

Database : EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_ntc:
 4: gb_est3:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_gss1:
 9: gb_gss2:
 .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
C 1	16.6	83.0	244	1	AV626231	AV626231 AV626231
C 2	16.6	83.0	406	5	BP094961	BP094961 BP094961
C 3	16.6	83.0	543	2	BE323149	BE323149 NF031A07P
C 4	16.6	83.0	638	7	CF664909	CF664909 PB2013XPF
C 5	15.8	79.0	501	7	CK098963	CK098963 A04SP11.5
C 6	15.6	78.0	124	1	AA471268	AA471268 PNTY2235 K
C 7	15.6	78.0	138	6	CD739260	CD739260 4027530 1
C 8	15.6	78.0	151	6	CD615018	CD615018 56009249J
C 9	15.6	78.0	161	6	CD615025	CD615025 56009298H
C 10	15.6	78.0	163	6	CB119089	CB119089 K-BST0165
C 11	15.6	78.0	164	6	CD615026	CD615026 56028980J
C 12	15.6	78.0	167	6	CD615017	CD615017 56009249H
C 13	15.6	78.0	171	6	CD731078	CD731078 4040029 1
C 14	15.6	78.0	173	6	CB119092	CB119092 K-BST0165
C 15	15.6	78.0	179	4	BM841467	BM841467 K-BST0118
C 16	15.6	78.0	180	6	CD615015	CD615015 56009048H
C 17	15.6	78.0	180	6	CD615016	CD615016 56009048J
C 18	15.6	78.0	182	6	CD615029	CD615029 56028996F
C 19	15.6	78.0	183	6	CD615030	CD615030 56028996H
C 20	15.6	78.0	192	2	BET75542	BET75542 MY-03-F-0
C 21	15.6	78.0	208	6	CD615022	CD615022 56028901J
C 22	15.6	78.0	208	7	D56165	D56165 HUM417H10B
C 23	15.6	78.0	214	7	CP644006	CP644006 K15 D04 P
C 24	15.6	78.0	221	6	CB122740	CB122740 K-BST0170

FEATURES

Source

PubMed

Comment

Title

Journal

Medline

Email:

Features

Organism

Nakamura, Y.

and Tabata, S.

Accession

AV626231.1

Version

EST.

Keywords

SOURCE

ORGANISM

Chlamydomonas reinhardtii

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadaceae; Chlamydomonas.

Chlamydomonas

Chlamydomonas

Chlamydomonas

Chlamydomonas

Chlamydomonas

Chlamydomonas

ALIGNMENTS

RESULT 1
 AV626231/c
 LOCUS AV626231 Chlamydomonas reinhardtii 5* to 0.04% CO2 Chlamydomonas
 DEFINITION reinhardtii cDNA clone LCM004907_r 5', mRNA sequence.
 ACCESSION AV626231
 VERSION AV626231.1
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii
 ORGANISM Chlamydomonas reinhardtii
 Chlamydomonadaceae; Chlamydomonas.
 Chlamydomonas
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1. (bases 1 to 244)

AUTHORS Asamizu, E., Miura, K., Kuroki, K., Inoue, Y., Fukuzawa, H., Ohyanaka, K., Nakamura, Y., and Tabata, S.

TITLE Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

DNA Res. 7 (5), 305-307 (2000)

JOURNAL DNA Res.

MEDLINE 11089944

PUBLMED 11089912

COMMENT Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp URL: http://www.kazusa.or.jp/en/plant/

FEATURES 1. 244 bp mRNA

/clone_xref="LCL004907_r"

/clone_id="Chlamydomonas reinhardtii 5* to 0.04% CO2"

/note="Vector: PBluescriptII SK; Site_1: EcoRI; Site_2: XbaI; The CDNA library was constructed from cells cultured

in a carbon stress acclimatized condition in which carbon

dioxide concentration in the bubbling gas was changed from

5% to 0.04%"

ORIGIN

305-307 (2000)

Source

PubMed

Contact

Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp URL: http://www.kazusa.or.jp/en/plant/

1. Location/Qualifiers

/organism="Chlamydomonas reinhardtii"

/mol_type="mRNA"

/strain="C9"

/db_xref="LCL004907_r"

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 133.901 Seconds

(without alignments)

6151.841 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: 1 gbcacrtcdgttgygg 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Post-processing: Minimum Match 0‡

Maximum Match 100§

Listing First 50 summaries

Database : GenBml:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_Pat:*

7: gb_ph:*

8: gb_Pl:*

9: gb_Pr:*

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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100§

Listing First 50 summaries

Result No.: Score

Match

Length

DB ID

Description

RESULT

1 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

GI:13537887

KEYWORDS

synthetic construct

ORGANISM

synthetic construct

other sequence; artificial sequences.

REFERENCE

1 Gioriano,G., dos Santos,J.P. and Mejean,V.

AUTHORS

TITLE

Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria.

JOURNAL

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES

Location/Qualifiers

1..17

Source

organism="synthetic construct"

/mol type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Patent: WO 0120030-A 23 22-MAR-2001;

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

Length 17;

DNA

RESULT

2 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

GI:13537887

KEYWORDS

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Location/Qualifiers

1..17

Source

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/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match

Best Local Similarity

100.0%

Pred. No. 7e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Length 17;

DNA

RESULT

3 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

GI:13537887

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/mol type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match

Best Local Similarity

100.0%

Pred. No. 7e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Length 17;

DNA

RESULT

4 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

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KEYWORDS

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FEATURES

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1..17

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/mol type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match

Best Local Similarity

100.0%

Pred. No. 7e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Length 17;

DNA

RESULT

5 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

GI:13537887

KEYWORDS

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JOURNAL

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES

Location/Qualifiers

1..17

Source

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/mol type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match

Best Local Similarity

100.0%

Pred. No. 7e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Length 17;

DNA

RESULT

6 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

GI:13537887

KEYWORDS

synthetic construct

ORGANISM

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FEATURES

Location/Qualifiers

1..17

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/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match

Best Local Similarity

100.0%

Pred. No. 7e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Length 17;

DNA

RESULT

7 AX098626

LOCUS

AX098626

DEFINITION

Sequence 23 from Patent WO0120030.

ACCESSION

AX098626.1

VERSION

GI:13537887

KEYWORDS

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ORGANISM

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other sequence; artificial sequences.

REFERENCE

1 Gioriano,G., dos Santos,J.P. and Mejean,V.

AUTHORS

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JOURNAL

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES

Location/Qualifiers

1..17

Source

organism="synthetic construct"

/mol type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match

Best Local Similarity

100.0%

Pred. No. 7e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Length 17;

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OM nucleic - nucleic search, using SW model

Run on: June 1, 2005, 22:48:55 ; Search time 16.9804 Seconds

(Without alignment)

5926.580 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: 1 gbaacrtcdgtyt-gygg 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1900s:*

2: Geneseqn2000s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	83.5	17	AAF79962	Aaf79962 PCR prime
c 2	14.2	83.5	223	AAAT21689	Aat21689 Human Gen
c 3	14.2	83.5	377	ABL163652	Ab163652 Breast ca
c 4	14.2	83.5	481	ACH36846	Ach36846 Human end
c 5	14.2	83.5	488	ACH34538	Ach34538 Human end
c 6	14.2	83.5	586	AAK92664	Aak92664 Human cDN
7	14.2	83.5	586	ADL28991	Adl28991 3' end of
c 8	14.2	83.5	812	AAA87695	Aaa87695 Human sec
c 9	14.2	83.5	812	AAC99855	Aac99855 Human sec
c 10	14.2	83.5	1559	ARS97017	Aab97017 DNA encod
c 11	14.2	83.5	1921	AAAS75108	Aas75108 DNA encod
c 12	14.2	83.5	2000	AAA23430	Aaa23430 cDNA encod
c 13	14.2	83.5	2077	ARCT76416	Aac76416 Human ORF
c 14	14.2	83.5	2261	AAK94291	Aak94291 Human ful
c 15	14.2	83.5	2261	ADL30907	Adl30907 Full leng
c 16	14.2	83.5	2366	AHH99489	Aah99489 Human pro
c 17	14.2	83.5	2403	ADD7297	Add7297 Human CGD
c 18	14.2	83.5	2443	AAS21272	Aas21272 Human cDN
c 19	14.2	83.5	2443	ACA03631	Aca03631 cDNA encod
c 20	14.2	83.5	2443	ABX89169	Abx89169 DNA encod

ALIGNMENTS

RESULT 1
ID AAF79962
XX AAF79962 standard; DNA; 17 BP.
XX DT 11-JUN-2001 (first entry)
XX DE PCR primer used to amplify trimethylamine N-oxide reductase genes.
XX KW torA gene; trimethylamine N-oxide reductase; flesh degradation;
XX KW spoilage bacteria; fish; crustacean; PCR primer; ss.
OS Synthetic.
XX PN WO200120030-A2.

XX WO200120030-A2.

XX 22-MAR-2001.

XX PD 22-MAR-2001.
XX PR 15-SEP-2000; 2000WO-FR002578.

XX PR 15-SEP-1999; 99PR-0011543.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Giordano G, Dos Santos J, Mejean V;

XX DR WPI; 2001-244932/25.

XX XX Detecting bacteria that cause flesh degradation in fish, for testing
PT freshness, comprises using probes or primers based on the trimethylamine
PT N-oxide reductase system.
XX Claim 7; Page 42; 91pp; French.
XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
PT torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
PT oxide reductase system. TorA nucleic acids are used for detecting, in a

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OM nucleic - nucleic search, using sw mode!

Run on: June 2, 2005, 08:20:11 ; Search time 5:25:038 Seconds
(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-23
Perfect score: 17
Sequence: 1 gbaacrtcdgtgygg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405558

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Result No.	Score	Query	Match	Length	DB ID	Description
c 1	14.2	83.5	2906	4	US-09-799-451-498	Sequence 498, App
c 2	13.2	77.6	25	1	US-08-173-510B-28	Sequence 28, App
c 3	13.2	77.6	25	1	US-08-45B-218-28	Sequence 28, App
c 4	13.2	77.6	25	2	US-08-45B-497-28	Sequence 28, App
c 5	13.2	77.6	25	4	US-08-45B-482B-28	Sequence 28, App
c 6	13.2	77.6	25	4	US-09-396-196G-54226	Sequence 54226, A
c 7	13.2	77.6	143	4	US-09-621-976-14486	Sequence 17691, A
c 8	13.2	77.6	348	4	US-09-621-976-17691	Sequence 9859, App
c 9	13.2	77.6	417	4	US-09-513-999C-9859	Sequence 92, App
c 10	13.2	77.6	825	1	US-08-173-510B-92	Sequence 90, App
c 11	13.2	77.6	825	1	US-08-45B-218-90	Sequence 92, App
c 12	13.2	77.6	825	2	US-08-45B-497-92	Sequence 92, App
c 13	13.2	77.6	825	4	US-08-45B-482B-92	Sequence 92, App
c 14	13.2	77.6	864	1	US-08-173-510B-94	Sequence 94, App
c 15	13.2	77.6	864	1	US-0-173-510B-96	Sequence 96, App
c 16	13.2	77.6	864	1	US-08-45B-218-92	Sequence 92, App
c 17	13.2	77.6	864	1	US-08-45B-218-94	Sequence 94, App
c 18	13.2	77.6	864	2	US-08-45B-497-94	Sequence 94, App
c 19	13.2	77.6	864	2	US-08-45B-497-96	Sequence 94, App
c 20	13.2	77.6	864	4	US-08-45B-482B-94	Sequence 96, App
c 21	13.2	77.6	864	4	US-0-45B-482B-96	Sequence 96, App
c 22	13.2	77.6	879	4	US-09-328-3931	Sequence 3931, App
c 23	13.2	77.6	40130	4	US-09-949-016-17227	Sequence 17275, A
c 24	13.2	77.6	112239	4	US-09-949-016-1314	Sequence 13144, A
c 25	13	76.5	576	4	US-09-765-29823	Sequence 23, App
c 26	13	76.5	579	3	US-09-387-341-191	Sequence 191, App
c 27	13	76.5	638	4	US-09-799-451-208	Sequence 208, App

ALIGNMENTS

RESULT 1
US-09-799-451-498/C
; Sequence 498, Application US/09799451
; Patent No. 6733969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radivoje T.
; TITLE OF INVENTION: No. 6733969el Nucleic Acids and
; POLypeptides
; FILE OF INVENTION: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOs: 948
; SOFTWARE: pt_Fl_genes Version 2.0
; SEQ ID NO 498
; FILE REFERENCE: 803
; LENGTH: 2906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: F
; NAME/REY: CDS
; LOCATION: (321)...(1898)
US-09-799-451-498

Query Match 83.5%; Score 14.2%; DB 4;
Best Local Similarity 70.6%; Pred. No. 1.6e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
1 GBCACRCCDGTGTTGGG 17
:||||:||||:||||:||

Qy

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 18.0919 Seconds

(without alignments)
 5776.400 Million cell updates/secTitle: US-10-088-117A-23
 Perfect score: 17

Sequence: 1 gbaacrtcdgtytgygg 17

Scoring table: IDANTITY_NUC
 Gapop 10_0 , Gapext 1_0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100‡

Listing first 50 summaries

Database : Published Applications_NA:+

```

1: /cgm2_6/ptodata/2/pubnpna/US07_PUBCOMB.seq:*
2: /cgm2_6/ptodata/2/pubnpna/PCT_NEW_PUB.seq:*
3: /cgm2_6/ptodata/2/pubnpna/US06_NEW_PUB.seq:*
4: /cgm2_6/ptodata/2/pubnpna/US05_PUBCOMB.seq:*
5: /cgm2_6/ptodata/2/pubnpna/US07_NEW_PUB.seq:*
6: /cgm2_6/ptodata/2/pubnpna/PCTUS_PUBCOMB.seq:*
7: /cgm2_6/ptodata/2/pubnpna/US05_NEW_PUB.seq:*
8: /cgm2_6/ptodata/2/pubnpna/US08_PUBCOMB.seq:*
9: /cgm2_6/ptodata/2/pubnpna/US09_NEW_PUBCOMB.seq:*
10: /cgm2_6/ptodata/2/pubnpna/US09C_PUBCOMB.seq:*
11: /cgm2_6/ptodata/2/pubnpna/US09_NEW_PUB.seq:*
12: /cgm2_6/ptodata/2/pubnpna/US10A_PUBCOMB.seq:*
13: /cgm2_6/ptodata/2/pubnpna/US10B_PUBCOMB.seq:*
14: /cgm2_6/ptodata/2/pubnpna/US10C_PUBCOMB.seq:*
15: /cgm2_6/ptodata/2/pubnpna/US10D_PUBCOMB.seq:*
16: /cgm2_6/ptodata/2/pubnpna/US10E_PUBCOMB.seq:*
17: /cgm2_6/ptodata/2/pubnpna/US10F_PUBCOMB.seq:*
18: /cgm2_6/ptodata/2/pubnpna/US10_NEW_PUB.seq:*
19: /cgm2_6/ptodata/2/pubnpna/US11_NEW_PUB.seq:*
20: /cgm2_6/ptodata/2/pubnpna/US11_NEW_PUB.seq:*
21: /cgm2_6/ptodata/2/pubnpna/US60_NEW_PUB.seq:*
22: /cgm2_6/ptodata/2/pubnpna/US60_NEW_PUBCOMB.seq:*
```

Sequence 57, App1

Sequence

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 114.318 Seconds
(without alignments)

5660.438 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: gbaacrtcdgtytggygg 17

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : EST:*

1: 9b_est1:*

2: 9b_est2:*

3: 9b_htc:*

4: 9b_est3:*

5: 9b_est4:*

6: 9b_est5:*

7: 9b_est6:*

8: 9b_gbs1:*

9: 9b_gbs2:*

Prid. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	83.5	220	6 C00843	C00843 HUMGS000313 H62165 yr47b12.81
C 2	14.2	83.5	265	7 H62165	AW044207 wyt1d10.x
C 3	14.2	83.5	318	2 AW044207	BMM987028 UI-H-C00-
C 4	14.2	83.5	320	5 BM987028	H87748 ys74907.81
C 5	14.2	83.5	329	7 H87748	BP057006 tk14150.81
C 6	14.2	83.5	338	2 AW953997	AW953997 EST365962
C 7	14.2	83.5	364	1 R32393	R32393 yh76c10.81
C 8	14.2	83.5	377	7 R32393	AA861050 ak21f03.s
C 9	14.2	83.5	385	1 AII952364	AI952364 wr72g08.x
C 10	14.2	83.5	391	1 AII952364	AI952364 wr72g08.x
C 11	14.2	83.5	395	2 AII619331	AI619331 705 MARC
C 12	14.2	83.5	424	1 AII200814	AII200814 qff62404.x
C 13	14.2	83.5	426	5 BQ322505	BQ322505 RC0-CS004
C 14	14.2	83.5	426	5 BQ322505	AII91901 qa92e01.s
C 15	14.2	83.5	427	1 AII91901	AA443280 ne39a10.8
C 16	14.2	83.5	428	1 AA443280	AA673019 v057405.r
C 17	14.2	83.5	432	1 AA673019	AA673019 v057405.r
C 18	14.2	83.5	446	1 AII867995	AII867995 ta0lh02.x
C 19	14.2	83.5	454	1 AII742802	AII742802 wg46d07.x
C 20	14.2	83.5	454	1 AII742802	AA443280 ne39a10.8
C 21	14.2	83.5	457	1 AII742802	AA443280 ne39a10.8
C 22	14.2	83.5	461	1 H01434	H01434 y199f11.81
C 23	14.2	83.5	467	1 AII521979	AII521979 ti7906.x
C 24	14.2	83.5	468	3 CNS059HDN	CNS059HDN Single re

ALIGNMENTS

RESULT 1
C00843/c

LOCUS HUMGS0003131 Human adult [K.Okubo] Homo sapiens cDNA, mRNA
DEFINITION HUMGS0003131 Human adult sequence.
ACCESSION C00843
VERSION C00843.1 GI:1433073
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 220)
AUTHORS Okubo, K.
TITLE Unpublished (1998)
JOURNAL
COMMENT Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
E-mail: kousaku@imcb.osaka-u.ac.jp
Tel: 06-877-5111 (ex.3315)
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see <http://www.imcb.osaka-u.ac.jp/bodymap>. The sequences of the clones represented by this GS sequences is also found there.

FEATURES
Source
1. Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:6006"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN
Query Match 83.5% Score 14.2; DB 6; Length 220;
Best Local Similarity 70.6%; Pred. No. 2.66+03;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;